

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chen, Ruoping
Dang, Huong T.
5 Liaw, Chen W.
Lin, I-Lin
- (ii) TITLE OF INVENTION: Human Orphan G Protein-Coupled Receptors
- (iii) NUMBER OF SEQUENCES: 74
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
15 (E) COUNTRY: USA
(F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
25 (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787
- (ix) TELECOMMUNICATION INFORMATION:
30 (A) TELEPHONE: (858)453-7200
(B) TELEFAX: (858)453-7210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

40 ATGGTCTTCT CGGCAGTGTT GACTGCGTTC CATACCGGGA CATCCAACAC AACATTTGTC 60

GTGTATGAAA ACACCTACAT GAATATTACA CTCCCTCCAC CATTCCAGCA TCCTGACCTC 120
AGTCCATTGC TTAGATATAG TTTTGAAACC ATGGCTCCCA CTGGTTTGAG TTCCTTGACC 180
GTGAATAGTA CAGCTGTGCC CACAACACCA GCAGCATTTA AGAGCCTAAA CTTGCCTCTT 240
CAGATCACCC TTTCTGCTAT AATGATATTC ATTCTGTTTG TGTCTTTTCT TGGGAACCTG 300
5 GTTGTTTGCC TCATGGTTTA CCAAAAAGCT GCCATGAGGT CTGCAATTAA CATCCTCCTT 360
GCCAGCCTAG CTTTTGCAGA CATGTTGCTT GCAGTGCTGA ACATGCCCTT TGCCCTGGTA 420
ACTATTCTTA CTACCCGATG GATTTTTGGG AAATCTTCT GTAGGGTATC TGCTATGTTT 480
TTCTGGTTAT TTGTGATAGA AGGAGTAGCC ATCCTGCTCA TCATTAGCAT AGATAGGTTT 540
CTTATTATAG TCCAGAGGCA GGATAAGCTA AACCCATATA GAGCTAAGGT TCTGATTGCA 600
10 GTTCTTTGGG CAACTTCCTT TTGTGTAGCT TTTCTTTTAG CCGTAGGAAA CCCCAGCCTG 660
CAGATACCTT CCCGAGCTCC CCAGTGTGTG TTTGGGTACA CAACCAATCC AGGCTACCAG 720
GCTTATGTGA TTTTGATTTT TCTCATTTCT TTCTTCATAC CCTTCCTGGT AATACTGTAC 780
TCATTTATGG GCATACTCAA CACCCTTCGG CACAATGCCT TGAGGATCCA TAGCTACCCT 840
GAAGGTATAT GCCTCAGCCA GGCCAGCAAA CTGGGTCTCA TGAGTCTGCA GAGACCTTTC 900
15 CAGATGAGCA TTGACATGGG CTTTAAACA CGTGCCTTCA CCACTATTTT GATTCTCTTT 960
GCTGTCTTCA TTGTCTGCTG GGCCCCATTC ACCACTTACA GCCTTGTTGGC
AACATTCAGT1020
AAGCACTTTT ACTATCAGCA CAACTTTTTT GAGATTAGCA CCTGGCTACT GTGGCTCTGC1080
TACCTCAAGT CTGCATTGAA TCCGCTGATC TACTACTGGA GGATTAAGAA ATTCCATGAT1140
20 GCTTGCCCTG ACATGATGCC TAAGTCCTTC AAGTTTTTGC CGCAGCTCCC TGGTCACACA1200
AAGCGACGGA TACGTCCTAG TGCTGTCTAT GTGTGTGGGG AACATCGGAC GGTGGTGTGA1260

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 419 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
1 5 10 15

Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro
 20 25 30
 Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
 35 40 45
 5 Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
 50 55 60
 Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
 65 70 75 80
 10 Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
 85 90 95
 Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
 100 105 110
 Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
 115 120 125
 15 Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
 130 135 140
 Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe
 145 150 155 160
 20 Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
 165 170 175
 Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
 180 185 190
 Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
 195 200 205
 25 Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
 210 215 220
 Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
 225 230 235 240
 30 Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
 245 250 255
 Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
 260 265 270
 Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
 275 280 285
 35 Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
 290 295 300
 Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe

09375076-060601

305 310 315 320
 Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
 325 330 335
 Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
 5 340 345 350
 Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
 355 360 365
 Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp
 370 375 380
 10 Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr
 385 390 395 400
 Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg
 405 410 415
 Thr Val Val
 15

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTAGCCA ACAGCTCCTC AACCAACAGT TCTGTTCTCC CGTGTCTGA CTACCGACCT 60
 25 ACCCACC GCC TGA CTTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCCTCAAC 120
 GCGCTAGCCC TCTGGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGTGTAC 180
 ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCACCTCT CGCTGCCCCG TCGTCTCTCC 240
 TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC 300
 TTCCAGATGA ACATGTACGG CAGCTGCATC TTCCTGATGC TCATCAACGT GGACCGCTAC 360
 30 GCCGCCATCG TGCACCCGCT GCGACTGCGC CACCTGCGGC GGCCCCGCGT GGC GCGGCTG 420
 CTCTGCCTGG GCGTGTGGGC GCTCATCCTG GTGTTTGCCG TGCCCGCCGC CCGCGTGCAC 480
 AGGCCCTCGC GTTGCCGCTA CCGGGACCTC GAGGTGCGCC TATGCTTCGA GAGCTTCAGC 540
 GACGAGCTGT GGAAAGGCAG GCTGCTGCCC CTCGTGCTGC TGGCCGAGGC GCTGGGCTTC 600

T09090"92052860

CTGCTGCCCC TGGCGGCGGT GGTCTACTCG TCGGGCCGAG TCTTCTGGAC GCTGGCGCGC 660
 CCCGACGCCA CGCAGAGCCA GCGGCGGCGG AAGACCGTGC GCCTCCTGCT GGCTAACCTC 720
 GTCATCTTCC TGCTGTGCTT CGTGCCCTAC AACAGCACGC TGGCGGTCTA CGGGCTGCTG 780
 CGGAGCAAGC TGGTGGCGGC CAGCGTGCCT GCCCGCGATC GCGTGCGCGG GGTGCTGATG 840
 5 GTGATGGTGC TGCTGGCCGG CGCCAACTGC GTGCTGGACC CGCTGGTGTA CTACTTTAGC 900
 GCCGAGGGCT TCCGCAACAC CCTGCGCGGC CTGGGCACTC CGCACCGGGC CAGGACCTCG 960
 GCCACCAACG GGACGCGGGC GCGCTCGCG CAATCCGAAA GTCCGCCGT CACCACCGAC1020
 GCCACCAGGC CGGATGCCGC CAGTCAGGGG CTGCTCCGAC CCTCCGACTC CCACTCTCTG1080
 TCTTCCTTCA CACAGTGTCC CCAGGATTCC GCCCTCTGA 1119

10 (5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro
 1 5 10 15
 20 Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val
 20 25 30
 Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
 35 40 45
 25 Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
 50 55 60
 Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
 65 70 75 80
 Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr
 85 90 95
 30 Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu
 100 105 110
 Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg
 115 120 125

0985076 0986601
 1099909 92054860

Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly
 130 135 140
 Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His
 145 150 155 160
 5 Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe
 165 170 175
 Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val
 180 185 190
 10 Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val
 195 200 205
 Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr
 210 215 220
 Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu
 225 230 235 240
 15 Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val
 245 250 255
 Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
 260 265 270
 20 Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
 275 280 285
 Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
 290 295 300
 Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
 305 310 315 320
 25 Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
 325 330 335
 Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
 340 345 350
 30 Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
 355 360 365
 Asp Ser Ala Leu
 370

(6) INFORMATION FOR SEQ ID NO:5:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

09875076-060601

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCCAACT CCACAGGGCT GAACGCCTCA GAAGTCGCAG GCTCGTTGGG GTTGATCCTG 60
GCAGCTGTCTG TGGAGGTGGG GGCAGTCTG GGCAACGGCG CGCTGCTGGT CGTGGTGCTG 120
5 CGCACGCCCG GACTGCGCGA CGCGCTCTAC CTGGCGCACC TGTGCGTCGT GGACCTGCTG 180
GCGGCCGCCT CCATCATGCC GCTGGGCCTG CTGGCCGCAC CGCCGCCCGG GCTGGGCCGC 240
GTGCGCCTGG GCCCCGCGCC ATGCCGCGCC GCTCGCTTCC TCTCCGCCG TCTGCTGCCG 300
GCCTGCACGC TCGGGGTGGC CGCACTTGGC CTGGCACGCT ACCGCCTCAT CGTGCACCCG 360
CTGCGGCCAG GCTCGCGGCC GCCGCCTGTG CTCGTGCTCA CCGCCGTGTG GGCCGCGGCG 420
10 GGA CTGCTGG GCGCGCTCTC CCTGCTCGGC CCGCCGCCCG CACCGCCCC TGCTCCTGCT 480
CGCTGCTCGG TCCTGGCTGG GGGCCTCGG CCCTTCCGGC CGCTCTGGGC CCTGCTGGCC 540
TTCGCGCTGC CCGCCCTCCT GCTGCTCGGC GCCTACGGCG GCATCTTCGT GGTGGCGCGT 600
CGCGCTGCCC TGAGGCCCCC ACGGCCGGCG CGCGGGTCCC GACTCCGCTC GGACTCTCTG 660
GATAGCCGCC TTTCCATCTT GCCGCCGCTC CGGCCTCGCC TGCCCGGGGG CAAGGCGGCC 720
15 CTGGCCCCAG CGCTGGCCGT GGGCCAATTT GCAGCCTGCT GGCTGCCTTA TGGCTGCGCG 780
TGCTTGGCGC CCGCAGCGCG GGCCGCGGAA GCCGAAGCGG CTGTCACCTG GGTGCCTTAC 840
TCGGCCTTCG CGGCTCAGCC CTTCTGTAC GGGCTGCTGC AGCGCCCCGT GCGCTTGGCA 900
CTGGGCCGCC TCTCTCGCCG TGCACTGCCT GGACCTGTGC GGGCCTGCAC TCCGAAGCC 960
TGGCAGCCGC GGGCACTCTT GCAATGCCTC CAGAGACCCC CAGAGGGCCC TGCCGTAGGC1020
20 CCTTCTGAGG CTCCAGAACA GACCCCCGAG TTGGCAGGAG GGCGGAGCCC CGCATACCAG1080
GGGCCACCTG AGAGTTCTCT CTCCTGA 1107

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 368 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

09875076 1060601

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu
 1 5 10 15
 Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn
 20 25 30
 5 Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
 35 40 45
 Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
 50 55 60
 10 Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
 65 70 75 80
 Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
 85 90 95
 Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
 100 105 110
 15 Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
 115 120 125
 Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
 130 135 140
 20 Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
 145 150 155 160
 Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
 165 170 175
 Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Leu Gly Ala Tyr
 180 185 190
 25 Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
 195 200 205
 Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
 210 215 220
 30 Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
 225 230 235 240
 Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro
 245 250 255
 Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu
 260 265 270
 35 Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe
 275 280 285
 Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu

09875076.060601

290 295 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala
305 310 315 320

5 Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly
325 330 335

Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala
340 345 350

Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser
355 360 365

10 (8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGAATCAT CTTTCTCATT TGGAGTGATC CTTGCTGTCC TGGCCTCCCT CATCATTGCT 60
ACTAACACAC TAGTGGCTGT GGCTGTGCTG CTGTTGATCC ACAAGAATGA TGGTGTTCAGT 120
20 CTCTGCTTCA CCTTGAATCT GGCTGTGGCT GACACCTTGA TTGGTGTGGC CATCTCTGGC 180
CTACTCACAG ACCAGCTCTC CAGCCCTTCT CGGCCACAC AGAAGACCCT GTGCAGCCTG 240
CGGATGGCAT TTGTCACTTC CTCCGCAGCT GCCTCTGTCC TCACGGTCAT GCTGATCACC 300
TTTGACAGGT ACCTTGCCAT CAAGCAGCCC TTCCGCTACT TGAAGATCAT GAGTGGGTTC 360
GTGGCCGGGG CCTGCATTGC CGGGCTGTGG TTAGTGTCTT ACCTCATTGG CTTCTCCCA 420
25 CTCGGAATCC CCATGTTCCA GCAGACTGCC TACAAAGGGC AGTGCAGCTT CTTTGCTGTA 480
TTTCACCCTC ACTTCGTGCT GACCCTCTCC TGC GTTGGCT TCTTCCCAGC CATGCTCCTC 540
TTTGCTTCT TCTACTGCGA CATGCTCAAG ATTGCCTCCA TGCACAGCCA GCAGATTCGA 600
AAGATGGAAC ATGCAGGAGC CATGGCTGGA GGTTATCGAT CCCACGGAC TCCCAGCGAC 660
TTCAAAGCTC TCCGTACTGT GTCTGTTCTC ATTGGGAGCT TTGCTCTATC CTGGACCCCC 720
30 TTCCTTATCA CTGGCATTGT GCAGGTGGCC TGCCAGGAGT GTCACCTCTA CCTAGTGCTG 780
GAACGGTACC TGTGGCTGCT CGGCGTGGGC AACTCCCTGC TCAACCCACT CATCTATGCC 840

09875076 060601

TATTGGCAGA AGGAGGTGCG ACTGCAGCTC TACCACATGG CCCTAGGAGT GAAGAAGGTG 900
 CTCACCTCAT TCCTCCTCTT TCTCTCGGCC AGGAATTGTG GCCCAGAGAG GCCCAGGGAA 960
 AGTTCCTGTC ACATCGTCAC TATCTCCAGC TCAGAGTTTG ATGGCTAA 1008

(9) INFORMATION FOR SEQ ID NO:8:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
 1 5 10 15
 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 15 20 25 30
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 20 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 25 100 105 110
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
 30 145 150 155 160
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
 165 170 175
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
 35 180 185 190

09875076 1060601

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
 195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220

5 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255

10 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300

15 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
 325 330 335

(10) INFORMATION FOR SEQ ID NO:9:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGACACTA CCATGGAAGC TGACCTGGGT GCCACTGGCC ACAGGCCCCG CACAGAGCTT 60

GATGATGAGG ACTCCTACCC CCAAGGTGGC TGGGACACGG TCTTCCTGGT GGCCCTGCTG 120

CTCCTTGGGC TGCCAGCCAA TGGGTTGATG GCGTGGCTGG CCGGCTCCCA GGCCCGGCAT 180

30 GGAGCTGGCA CGCGTCTGGC GCTGCTCCTG CTCAGCCTGG CCCTCTCTGA CTTCTTGTTT 240

CTGGCAGCAG CGGCCTTCCA GATCCTAGAG ATCCGGCATG GGGGACACTG GCCGCTGGGG 300

ACAGCTGCCT GCCGCTTCTA CTACTTCCTA TGGGGCGTGT CCTACTCCTC CGGCCTCTTC 360

CTGCTGGCCG CCCTCAGCCT CGACCGCTGC CTGCTGGCGC TGTGCCCACA CTGGTACCCT 420

GGGCACCGCC CAGTCCGCCT GCCCCTCTGG GTCTGCGCCG GTGTCTGGGT GCTGGCCACA 480

09875076 "050601"

CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCCG TCTGGTGGTA CGACCTGGTC 540
ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTGCTGA GGATGCTGGA GGTCTGGGG 600
GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT 660
CGCACCTGCC ACCGCCAACA GCAGCCCGCA GCCTGCCGGG GCTTCGCCCC TGTGGCCAGG 720
5 ACCATTCTGT CAGCCTATGT GGTCTGAGG CTGCCCTACC AGCTGGCCCA GCTGCTCTAC 780
CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC 840
GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC 900
GACCTCCGGA CCCTGCTGCG CTCCGTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG 960
CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCAAC1020
10 CTGCCAGAGC CGATGGCAGA GGCCAGTCA CAGATGGATC CTGTGGCCCA GCCTCAGGTG1080
AACCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC1140
CAGCCACAGT CGGATCCCAC AGCCAGCCA CAGCTGAACC TCATGGCCCA GCCACAGTCA1200
GATTCTGTGG CCCAGCCACA GGCAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT1260
TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCCAT CCTCGCATCC TACCCAGGG1320
15 GCCCTTGAGG ACCCAGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCCG1380
CCAGAGGCGG CCCCAGGCGC AGGCCCCACG TGA 1413

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 468 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro
1 5 10 15
Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
20 25 30
30 Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly
35 40 45
Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr

	50	55	60
	Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe		
	65	70	75 80
5	Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His		
	85	90	95
	Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly		
	100	105	110
	Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp		
	115	120	125
10	Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro		
	130	135	140
	Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr		
	145	150	155 160
15	Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp		
	165	170	175
	Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser		
	180	185	190
	Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu		
	195	200	205
20	Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln		
	210	215	220
	Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile		
	225	230	235 240
25	Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu		
	245	250	255
	Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp		
	260	265	270
	Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu		
	275	280	285
30	Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu		
	290	295	300
	Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro		
	305	310	315 320
35	Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly		
	325	330	335
	Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro		
	340	345	350

09875076 "060601"

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
370 375 380

5 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
405 410 415

10 Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser
420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala
435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly
450 455 460

15 Ala Gly Pro Thr
465

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25 ATGTCAGGGA TGGAAAACT TCAGAATGCT TCCTGGATCT ACCAGCAGAA ACTAGAAGAT 60
 CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG 120
 CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGTG GGTGGGGGTC 180
 ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCCACC 240
 AACTACTACC TCTTCAGCCT GCGGGTCTCT GACCTCCTGG TCCTGCTCCT TGGAAATGCCC 300
 30 CTGGAGGTCT ATGAGATGTG GCGCAACTAC CCTTTCTTGT TCGGGCCCGT GGGCTGCTAC 360
 TTCAAGACGG CCCTCTTTGA GACCGTGTGC TTCGCCTCCA TCCTCAGCAT CACCACCGTC 420
 AGCGTGGAGC GCTACGTGGC CATCCTACAC CCGTTCGCG CCAAACCTGCA GAGCACCCGG 480
 CGCCGGGCCC TCAGGATCCT CGGCATCGTC TGGGGCTTCT CCGTGCTCTT CTCCCTGCCC 540

109675076.060604
 T09090" 9/205/2060

AACACCAGCA TCCATGGCAT CAAGTTCCAC TACTTCCCCA ATGGGTCCCT GGTCCCAGGT 600
 TCGGCCACCT GTACGGTCAT CAAGCCCATG TGGATCTACA ATTTTCATCAT CCAGGTCACC 660
 TCCTTCCTAT TCTACCTCCT CCCCATGACT GTCATCAGTG TCCTCTACTA CCTCATGGCA 720
 CTCAGACTAA AGAAAGACAA ATCTCTTGAG GCAGATGAAG GGAATGCAAA TATTCAAAGA 780
 5 CCCTGCAGAA AATCAGTCAA CAAGATGCTG TTTGTCTTGG TCTTAGTGTT TGCTATCTGT 840
 TGGGCCCCGT TCCACATTGA CCGACTCTTC TTCAGCTTTG TGGAGGAGTG GAGTGAATCC 900
 CTGGCTGCTG TGTTC AACCT CGTCCATGTG GTGTCAGGTG TCTTCTTCTA CCTGAGCTCA 960
 GCTGTCAACC CCATTATCTA TAACCTACTG TCTCGCCGCT TCCAGGCAGC ATTCCAGAAT1020
 GTGATCTCTT CTTTCCACAA ACAGTGGCAC TCCCAGCATG ACCCACAGTT GCCACCTGCC1080
 10 CAGCGGAACA TCTTCTTGAC AGAATGCCAC TTTGTGGAGC TGACCGAAGA TATAGGTCCC1140
 CAATTCCCAT GTCAGTCATC CATGCACAAC TCTCACCTCC CAACAGCCCT CTCTAGTGAA1200
 CAGATGTCAA GAACAAACTA TCAAAGCTTC CACTTTAACA AAACCTGA 1248

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ser	Gly	Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	1	5	10	15	
Lys	Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	20	25	30		
Leu	Ala	Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	25	35	40	45	
Ser	Val	Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	50	55	60		
Leu	Val	Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	30	65	70	75	80
Asn	Tyr	Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	85	90	95		

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
 100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
 115 120 125

5 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
 130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
 145 150 155 160

10 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
 165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
 180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
 195 200 205

15 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
 210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
 225 230 235 240

20 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
 245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
 260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
 275 280 285

25 Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val
 290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
 305 310 315 320

30 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
 325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
 340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
 355 360 365

35 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
 370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
 385 390 395 400

09875076.060601

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
405 410 415

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA CTAATAGCAC AATCAATTTA TCACTAAGCA CTCGTGTTAC TTTAGCATT 60
TTTATGTCCT TAGTAGCTTT TGCTATAATG CTAGGAAATG CTTTGGTCAT TTTAGCTTTT 120
GTGGTGGACA AAAACCTTAG ACATCGAAGT AGTTATTTTT TTCTTAACTT GGCCATCTCT 180
GACTTCTTTG TGGGTGTGAT CTCCATTCTT TTGTACATCC CTCACACGCT GTTCGAATGG 240
15 GATTTTGGAA AGGAAATCTG TGTATTTTGG CTCACTACTG ACTATCTGTT ATGTACAGCA 300
TCTGTATATA ACATTGTCCT CATCAGCTAT GATCGATACC TGTCAGTCTC AAATGCTGTG 360
TCTTATAGAA CTCAACATAC TGGGGTCTTG AAGATTGTTA CTCTGATGGT GGCCGTTTGG 420
GTGCTGGCCT TCTTAGTGAA TGGGCCAATG ATTCTAGTTT CAGAGTCTTG GAAGGATGAA 480
GGTAGTGAAT GTGAACCTGG ATTTTTTTTCG GAATGGTACA TCCTTGCCAT CACATCATTC 540
20 TTGGAATTCG TGATCCCAGT CATCTTAGTC GCTTATTTCA ACATGAATAT TTATTGGAGC 600
CTGTGGAAGC GTGATCATCT CAGTAGGTGC CAAAGCCATC CTGGACTGAC TGCTGTCTCT 660
TCCAACATCT GTGGACACTC ATTCAGAGGT AGACTATCTT CAAGGAGATC TCTTCTGCA 720
TCGACAGAAG TTCCTGCATC CTTTCATTCA GAGAGACAGA GGAGAAAGAG TAGTCTCATG 780
TTTTCTCTCA GAACCAAGAT GAATAGCAAT ACAATTGCTT CCAAATGGG TTCCTTCTCC 840
25 CAATCAGATT CTGTAGCTCT TCACCAAAGG GAACATGTTG AACTGCTTAG AGCCAGGAGA 900
TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTTGCTG TTTGCTGGGC TCCATATTCT 960
CTGTTCACAA TTGTCCTTTC ATTTTATTCC TCAGCAACAG GTCCTAAATC AGTTTGGTAT 1020
AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTTGTCA ATCCTCTTTT GTATCCATTG 1080
TGTCACAAGC GCTTTCAAAA GGCTTTCTTG AAAATATTTT GTATAAAAAA GCAACCTCTA 1140
30 CCATCACAAAC ACAGTCGGTC AGTATCTTCT TAA 1173

09875075-060601

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 5 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
 10 1 5 10 15

Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
 20 25 30

Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
 35 40 45

15 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
 50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
 65 70 75 80

20 Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
 85 90 95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
 100 105 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
 115 120 125

25 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
 130 135 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
 145 150 155 160

30 Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
 165 170 175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr
 180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser
 195 200 205

35 Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys
 210 215 220

T09090" 92052860

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala
 225 230 235 240
 Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys
 245 250 255
 5 Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile
 260 265 270
 Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His
 275 280 285
 10 Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser
 290 295 300
 Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser
 305 310 315 320
 Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys
 325 330 335
 15 Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe
 340 345 350
 Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala
 355 360 365
 20 Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His
 370 375 380
 Ser Arg Ser Val Ser Ser
 385 390

(16) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGCGAACG CGAGCGAGCC GGGTGGCAGC GGCGGCGGCG AGGCGGCCGC CCTGGGCCTC 60
 AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTCGCG 120
 CTGCTGATCG TCGGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG 180
 TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCCTCCCGG CCGTCATGCT GGCGGCGCGG 240
 35 CGTGCGGCGG CCGCGGCGGG GGCGCCGCGG GGCGCGCTGG GCTGCAAGCT GCTCGCCTTC 300

D9875076 "060601"

CTGGCCGCGC TCTTCTGCTT CCACGCCGCC TTCCTGCTGC TGGGCGTGGG CGTCACCCGC 360
 TACCTGGCCA TCGCGACCA CCGCTTCTAT GCAGAGCGCC TGGCCGGCTG GCCGTGCGCC 420
 GCCATGCTGG TGTGCGCCG CTGGGCGCTG GCGCTGGCCG CGGCCTTCCC GCCAGTGCTG 480
 GACGGCGGTG GCGACGACGA GGACGCGCCG TGCGCCCTGG AGCAGCGGCC CGACGGCGCC 540
 5 CCCGGCGCGC TGGGCTTCCT GCTGCTGCTG GCCGTGGTGG TGGGCGCCAC GCACCTCGTC 600
 TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TGCGGCCCCG GCGCCTGGTG 660
 CCCGCCGTCA GCCACGACTG GACCTTCCAC GGCCCGGGCG CCACCGGCCA GCGGGCCGCC 720
 AACTGGACGG CGGGCTTCGG CCGCGGGCCC ACGCCGCCCG CGCTTGTGGG CATCCGGCCC 780
 GCAGGGCCGG GCCGCGGCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGGAGAAG 840
 10 AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900
 GTCGTGGCCA GCTACCTGCG GGTCTTGGTG CGGCCCCGCG CCGTCCCCCA GGCCTACCTG 960
 ACGGCCTCCG TGTGGCTGAC CTTGCGCGAG GCCGGCATCA ACCCGTCGT GTGCTTCCTC1020
 TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCCCAGTTCC CCTGCTGCCA GAGCCCCCGG1080
 ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128

15 (17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
 1 5 10 15
 25 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
 20 25 30
 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
 35 40 45
 30 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
 50 55 60
 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
 65 70 75 80

T0905076-050504

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
 85 90 95
 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
 100 105 110
 5 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
 115 120 125
 Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
 130 135 140
 10 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
 145 150 155 160
 Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
 165 170 175
 Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
 180 185 190
 15 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
 195 200 205
 His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
 210 215 220
 20 His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala
 225 230 235 240
 Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
 245 250 255
 Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
 260 265 270
 25 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
 275 280 285
 Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
 290 295 300
 30 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
 305 310 315 320
 Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
 325 330 335
 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
 340 345 350
 35 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
 355 360 365
 Asp Leu Lys Gly Ile Gly Leu

009090" 92052860

370

375

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 ATGAACACCA CAGTGATGCA AGGCTTCAAC AGATCTGAGC GGTGCCCCAG AGACACTCGG 60
ATAGTACAGC TGGTATTCCC AGCCCTCTAC ACAGTGGTTT TCTTGACCGG CATCCTGCTG 120
AATACTTTGG CTCTGTGGGT GTTTGTTTAC ATCCCCAGCT CCTCCACCTT CATCATCTAC 180
CTCAAAAACA CTTTGGTGGC CGACTTGATA ATGACACTCA TGCTTCCTTT CAAAATCCTC 240
TCTGACTCAC ACCTGGCACC CTGGCAGCTC AGAGCTTTTG TGTGTCGTTT TTCTTCGGTG 300
15 ATATTTTATG AGACCATGTA TGTGGGCATC GTGCTGTTAG GGCTCATAGC CTTTGACAGA 360
TTCCTCAAGA TCATCAGACC TTTGAGAAAT ATTTTCTAA AAAACCTGT TTTTGCAAAA 420
ACGGTCTCAA TCTTCATCTG GTTCTTTTTG TTCTTCATCT CCCTGCCAAA TACGATCTTG 480
AGCAACAAGG AAGCAACACC ATCGTCTGTG AAAAAGTGTG CTTCTTAAA GGGGCCTCTG 540
GGGCTGAAAT GGCATCAAAT GGTAAATAAC ATATGCCAGT TTATTTTCTG GACTGTTTTT 600
20 ATCCTAATGC TTGTGTTTTA TGTGGTTATT GCAAAAAAAG TATATGATTC TTATAGAAAG 660
TCCAAAAGTA AGGACAGAAA AAACAACAAA AAGCTGGAAG GCAAAGTATT TGTTGTCGTG 720
GCTGTCTTCT TTGTGTGTTT TGCTCCATTT CATTTTGCCA GAGTTCCATA TACTCACAGT 780
CAAACCAACA ATAAGACTGA CTGTAGACTG CAAAATCAAC TGTTTATTGC TAAAGAAACA 840
ACTCTCTTTT TGGCAGCAAC TAACATTTGT ATGGATCCCT TAATATACAT ATTCTTATGT 900
25 AAAAAATTCA CAGAAAAGCT ACCATGTATG CAAGGGAGAA AGACCACAGC ATCAAGCCAA 960
GAAATCATA GCAGTCAGAC AGACAACATA ACCTTAGGCT GA 1002

(19) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

5 Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
 1 5 10 15
 Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
 20 25 30
 Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
 35 40 45
 10 Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
 50 55 60
 Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
 65 70 75 80
 15 Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
 85 90 95
 Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
 100 105 110
 Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
 115 120 125
 20 Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
 130 135 140
 Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
 145 150 155 160
 25 Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
 165 170 175
 Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
 180 185 190
 Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
 195 200 205
 30 Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
 210 215 220
 Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
 225 230 235 240
 35 Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
 245 250 255

09875076-050601

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

5 Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

10 Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
325 330

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA 60

20 TCAGCTTATG TGAAGCTGGT ACTGCTGGGA CTGATTATGT GCGTGAGCCT GGCGGGTAAC 120

GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCCTGC ACAAGGCTCC TTACTACTTC 180

CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTTGTGCTG 240

GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGCAC TCAGCTGCAA GATTGTGGCC 300

TTTATGGCCG TGCTCTTTTG CTTCCATGCG GCCTTCATGC TGTTCATGCAT CAGCGTCACC 360

25 CGCTACATGG CCATCGCCCA CCACCGCTTC TACGCCAAGC GCATGACACT CTGGACATGC 420

GCGGCTGTCA TCTGCATGGC CTGGACCCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT 480

GACGTGGGCA CCTACAAGTT TATTCGGGAG GAGGACCAGT GCATCTTTGA GCATCGCTAC 540

TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC 600

CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG 660

30 CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCGGGGC CACCGGCCAG 720

GCTGCTGCCA ACTGGATCGC CGGCTTTGGC CGTGGGCCCC TGCCACCAAC CCTGCTGGGT 780

ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTCAAGGGT 840

GAAAAGCAGC TGGGCCGCAT GTTCTACGCG ATCACACTGC TCTTTCTGCT CCTCTGGTCA 900
 CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC 960
 TACCTGGCCA CTGCTGTTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC1020
 TTCTGTCTCA ACAAGGACCT CAAGAAGTGC CTGACCACTC ACGCCCCCTG CTGGGGCACA1080
 5 GGAGGTGCCC CGGCTCCAG AGAACCTAC TGTGTCATGT GA 1122

(21) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
 1 5 10 15
 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30
 Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60
 Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
 65 70 75 80
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140
 Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160
 Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 5 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 10 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 15 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320
 20 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr
 340 345 350
 Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365
 25 Pro Tyr Cys Val Met
 370

(22) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1053 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC 60
 ACTTATGACT ACAGTCAATA TGAATTGATC TGTATCAAAG AAGATGTCAG AGAATTTGCA 120

1050501 050507 92052860

AAAGTTTTCC TCCCTGTATT CCTCACAATA GCTTTCGTCA TTGGACTTGC AGGCAATTCC 180
 ATGGTAGTGG CAATTTATGC CTATTACAAG AACAGAGAA CAAAACAGA TGTGTACATC 240
 CTGAATTTGG CTGTAGCAGA TTTACTCCTT CTATTCACCTC TGCCTTTTTG GGCTGTTAAT 300
 GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC CTTGTACACA 360
 5 CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGCATCA GCATAGACAG ATATGTGGCA 420
 GTAACATAATG TCCCAGCCA ATCAGGAGTG GGAAAACCAT GCTGGATCAT CTGTTTCTGT 480
 GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCAGCTGG TTTTTATAC AGTAAATGAC 540
 AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT 600
 CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG GGTGTGCTAC 660
 10 TTTATCACGG CAAGGACACT CATGAAGATG CAAACATTA AAATATCTCG ACCCCTAAAA 720
 GTTCTGCTCA CAGTCGTTAT AGTTTTCAAT GTCACCAAC TGCCTTATAA CATTGTCAAG 780
 TTCTGCCGAG CCATAGACAT CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC 840
 ATGGACATCG CCATCCAAGT CACAGAAAGC ATTGCACTCT TTCACAGCTG CCTCAACCCA 900
 ATCCTTTATG TTTTATGGG AGCATCTTTC AAAAAGTACG TTATGAAAGT GGCCAAGAAA 960
 15 TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT TTCCTTTTGA TTCTGAGGGT 1020
 CCTACAGAGC CAACCAAGTAC TTTTAGCATT TAA 1053

(23) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
 1 5 10 15
 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
 20 25 30
 30 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45
 Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala

	50	55	60
	Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile		
	65	70	75 80
5	Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe		
	85	90	95
	Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys		
	100	105	110
	Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln		
	115	120	125
10	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val		
	130	135	140
	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys		
	145	150	155 160
15	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr		
	165	170	175
	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu		
	180	185	190
	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly		
	195	200	205
20	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala		
	210	215	220
	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys		
	225	230	235 240
25	Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr		
	245	250	255
	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile		
	260	265	270
	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr		
	275	280	285
30	Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val		
	290	295	300
	Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys		
	305	310	315 320
35	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe		
	325	330	335
	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		
	340	345	350

09875076 060601

(24) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCCGT GGGCCTCCCT GGGCCTCTCC 60
10 GCCAAGACCT GCAACAACGT GTCCTTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC 120
AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCCTGTCTG 180
CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAACTG 240
CTGTACACAG GCACGCTGCC ACTCTGGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC 300
CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC 360
15 ATCCTCTTCC TGTGCTGCAT CTCCTGCGAC CGCTTCGTGG CCGTGGTGTA CGCGCTGGAG 420
AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTTCATCTC 480
GTCTGGGATCG TTCACTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG 540
CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTTGCC 600
ATCCCTCTCT CCATCATCGC CTTACCAAC CACCGGATTT TCAGGAGCAT CAAGCAGAGC 660
20 ATGGGCTTAA GCGCTGCCCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC 720
ATCTTCCTAG TCTGCTTCGC CCCGTACCAC CTGGTTCTCC TCGTCAAAGC CGCTGCCTTT 780
TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC 840
TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCCAT TATCTACGTG 900
CTGGCCACGG ACCATTCCCG CCAAGAAGTG TCCAGAATCC ATAAGGGGTG GAAAGAGTGG 960
25 TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG1020
CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCCG TGCACCCACC AGGGTCACCA1080
TGCCCTGCAA AGAGGCTGAT TGAGGAGTCC TGCTGA 1116

(25) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 371 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	Met	Pro	Gly	Asn	Ala	Thr	Pro	Val	Thr	Thr	Thr	Ala	Pro	Trp	Ala	Ser	
	1				5					10					15		
	Leu	Gly	Leu	Ser	Ala	Lys	Thr	Cys	Asn	Asn	Val	Ser	Phe	Glu	Glu	Ser	
				20				25						30			
10	Arg	Ile	Val	Leu	Val	Val	Val	Tyr	Ser	Ala	Val	Cys	Thr	Leu	Gly	Val	
			35					40					45				
	Pro	Ala	Asn	Cys	Leu	Thr	Ala	Trp	Leu	Ala	Leu	Leu	Gln	Val	Leu	Gln	
		50					55					60					
	Gly	Asn	Val	Leu	Ala	Val	Tyr	Leu	Leu	Cys	Leu	Ala	Leu	Cys	Glu	Leu	
15	65					70				75					80		
	Leu	Tyr	Thr	Gly	Thr	Leu	Pro	Leu	Trp	Val	Ile	Tyr	Ile	Arg	Asn	Gln	
				85					90					95			
	His	Arg	Trp	Thr	Leu	Gly	Leu	Leu	Ala	Ser	Lys	Val	Thr	Ala	Tyr	Ile	
			100						105					110			
20	Phe	Phe	Cys	Asn	Ile	Tyr	Val	Ser	Ile	Leu	Phe	Leu	Cys	Cys	Ile	Ser	
			115					120					125				
	Cys	Asp	Arg	Phe	Val	Ala	Val	Val	Tyr	Ala	Leu	Glu	Ser	Arg	Gly	Arg	
		130					135					140					
	Arg	Arg	Arg	Arg	Thr	Ala	Ile	Leu	Ile	Ser	Ala	Cys	Ile	Phe	Ile	Leu	
25	145					150				155						160	
	Val	Gly	Ile	Val	His	Tyr	Pro	Val	Phe	Gln	Thr	Glu	Asp	Lys	Glu	Thr	
					165					170					175		
	Cys	Phe	Asp	Met	Leu	Gln	Met	Asp	Ser	Arg	Ile	Ala	Gly	Tyr	Tyr	Tyr	
				180					185					190			
30	Ala	Arg	Phe	Thr	Val	Gly	Phe	Ala	Ile	Pro	Leu	Ser	Ile	Ile	Ala	Phe	
			195					200					205				
	Thr	Asn	His	Arg	Ile	Phe	Arg	Ser	Ile	Lys	Gln	Ser	Met	Gly	Leu	Ser	
		210					215					220					
	Ala	Ala	Gln	Lys	Ala	Lys	Val	Lys	His	Ser	Ala	Ile	Ala	Val	Val	Val	
35	225					230					235					240	

05875076.060601

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
 245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
 260 265 270

5 Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
 275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
 290 295 300

10 His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp
 305 310 315 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
 325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
 340 345 350

15 Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
 355 360 365

Glu Ser Cys
 370

(26) INFORMATION FOR SEQ ID NO:25:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGCGAACT ATAGCCATGC AGCTGACAAC ATTTTGCAAA ATCTCTCGCC TCTAACAGCC 60
 TTTCTGAAAC TGACTTCCTT GGGTTTCATA ATAGGAGTCA GCGTGGTGGG CAACCTCCTG 120
 ATCTCCATTT TGCTAGTGAA AGATAAGACC TTGCATAGAG CACCTTACTA CTTCTGTGTTG 180
 30 GATCTTTGCT GTTCAGATAT CCTCAGATCT GCAATTTGTT TCCCATTTGT GTTCAACTCT 240
 GTCAAAAATG GCTCTACCTG GACTTATGGG ACTCTGACTT GCAAAGTGAT TGCCTTTCTG 300
 GGGGTTTTGT CCTGTTTCCA CACTGCTTTC ATGCTCTTCT GCATCAGTGT CACCAGATAC 360
 TTAGCTATCG CCCATCACCG CTTCTATACA AAGAGGCTGA CCTTTTGGAC GTGTCTGGCT 420
 GTGATCTGTA TGGTGTGGAC TCTGTCTGTG GCCATGGCAT TTCCCCGGT TTTAGACGTG 480

0985076.060601

GGCACTTACT CATTCAATTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCTTCAGG 540
 GCTAATGATT CCTTAGGATT TATGCTGCTT CTTGCTCTCA TCCTCCTAGC CACACAGCTT 600
 GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT 660
 GTAGCAGCAG TCAGCCAGAA CTGGACTTTT CATGGTCTCTG GAGCCAGTGG CCAGGCAGCT 720
 5 GCCAATTGGC TAGCAGGATT TGAAGGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG 780
 CAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACGAGTT CAAAATGGAG 840
 AAAAGAATCA GCAGAAATGT CTATATAATG ACTTTTCTGT TTCTAACCTT GTGGGGCCCC 900
 TACCTGGTGG CCTGTTATTG GAGAGTTTTT GCAAGAGGGC CTGTAGTACC AGGGGGATTT 960
 CTAACAGCTG CTGTCTGGAT GAGTTTTGCC CAAGCAGGAA TCAATCCTTT TGTCTGCATT1020
 10 TTCTCAAACA GGGAGCTGAG GCGCTGTTTC AGCACAACCC TTCTTTACTG CAGAAAATCC1080
 AGGTTACCAA GGGAACCTTA CTGTGTTATA TGA 1113

(27) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30
 25 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80
 30 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu

09375076 060601

	100	105	110
	Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe 115 120 125		
5	Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met 130 135 140		
	Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val 145 150 155 160		
	Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His 165 170 175		
10	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala 180 185 190		
	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe 195 200 205		
15	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val 210 215 220		
	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala 225 230 235 240		
	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu 245 250 255		
20	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu 260 265 270		
	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr 275 280 285		
25	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala 290 295 300		
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe 305 310 315 320		
	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro 325 330 335		
30	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr 340 345 350		
	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys 355 360 365		
35	Val Ile 370		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGGTCC CGAACAGCAC CGGCCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG 60
GCGATCGCGG TGGCCCTGCC CGTGGTGTAC TCGCTGGTGG CGGCGGTCAG CATCCCGGGC 120
10 AACCTCTTCT CTCTGTGGGT GCTGTGCCGG CGCATGGGGC CCAGATCCCC GTCGGTCATC 180
TTCATGATCA ACCTGAGCGT CACGGACCTG ATGCTGGCCA GCGTGTTGCC TTTCCAAATC 240
TACTACCATT GCAACCGCCA CCACTGGGTA TTCGGGGTGC TGCTTTGCAA CGTGGTGACC 300
GTGGCCTTTT ACGCAAACAT GTATTCCAGC ATCCTCACCA TGACCTGTAT CAGCGTGGAG 360
CGCTTCCTGG GGGTCCTGTA CCCGCTCAGC TCCAAGCGCT GCGCCGCCCG TCGTTACGCG 420
15 GTGGCCGCGT GTGCAGGGAC CTGGCTGCTG CTCCTGACCG CCCTGTGCCC GCTGGCGCGC 480
ACCGATCTCA CCTACCCGGT GCACGCCCTG GGCATCATCA CCTGCTTCGA CGTCCTCAAG 540
TGGACGATGC TCCCCAGCGT GGCCATGTGG GCCGTGTTCC TCTTCACCAT CTTCATCCTG 600
CTGTTCTCTA TCCCGTTCGT GATCACCGTG GCTTGTTACA CGGCCACCAT CCTCAAGCTG 660
TTGCGCACGG AGGAGGCGCA CGGCCGGGAG CAGCGGAGGC GCGCGGTGGG CCTGGCCGCG 720
20 GTGGTCTTGC TGGCCTTTGT CACCTGCTTC GCCCCAACA ACTTCGTGCT CCTGGCGCAC 780
ATCGTGAGCC GCCTGTTCTA CGGCAAGAGC TACTACCAGC TGTACAAGCT CACGCTGTGT 840
CTCAGCTGCC TCAACAACCTG TCTGGACCCG TTTGTTTATT ACTTTGCGTC CCGGGAATTC 900
CAGCTGCGCC TCGGGAATA TTTGGGCTGC CGCCGGGTGC CCAGAGACAC CCTGGACACG 960
CGCCGCGAGA GCCTCTTCTC CGCCAGGACC ACGTCCGTGC GCTCCGAGGC CGGTGCGCAC1020
25 CCTGAAGGGA TGGAGGGAGC CACCAGGCCC GGCCTCCAGA GGCAGGAGAG TGTGTTCTGA1080

(29) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
30 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

	Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met	
	1				5					10					15		
5	Leu	Arg	Asn	Pro	Ala	Ile	Ala	Val	Ala	Leu	Pro	Val	Val	Tyr	Ser	Leu	
				20					25					30			
	Val	Ala	Ala	Val	Ser	Ile	Pro	Gly	Asn	Leu	Phe	Ser	Leu	Trp	Val	Leu	
				35				40					45				
10	Cys	Arg	Arg	Met	Gly	Pro	Arg	Ser	Pro	Ser	Val	Ile	Phe	Met	Ile	Asn	
		50					55					60					
	Leu	Ser	Val	Thr	Asp	Leu	Met	Leu	Ala	Ser	Val	Leu	Pro	Phe	Gln	Ile	
	65					70				75					80		
	Tyr	Tyr	His	Cys	Asn	Arg	His	His	Trp	Val	Phe	Gly	Val	Leu	Leu	Cys	
					85					90					95		
15	Asn	Val	Val	Thr	Val	Ala	Phe	Tyr	Ala	Asn	Met	Tyr	Ser	Ser	Ile	Leu	
					100				105					110			
	Thr	Met	Thr	Cys	Ile	Ser	Val	Glu	Arg	Phe	Leu	Gly	Val	Leu	Tyr	Pro	
				115				120					125				
20	Leu	Ser	Ser	Lys	Arg	Trp	Arg	Arg	Arg	Arg	Tyr	Ala	Val	Ala	Ala	Cys	
		130					135					140					
	Ala	Gly	Thr	Trp	Leu	Leu	Leu	Leu	Thr	Ala	Leu	Cys	Pro	Leu	Ala	Arg	
	145					150					155					160	
	Thr	Asp	Leu	Thr	Tyr	Pro	Val	His	Ala	Leu	Gly	Ile	Ile	Thr	Cys	Phe	
					165					170					175		
25	Asp	Val	Leu	Lys	Trp	Thr	Met	Leu	Pro	Ser	Val	Ala	Met	Trp	Ala	Val	
				180					185					190			
	Phe	Leu	Phe	Thr	Ile	Phe	Ile	Leu	Leu	Phe	Leu	Ile	Pro	Phe	Val	Ile	
			195					200					205				
30	Thr	Val	Ala	Cys	Tyr	Thr	Ala	Thr	Ile	Leu	Lys	Leu	Leu	Arg	Thr	Glu	
		210					215					220					
	Glu	Ala	His	Gly	Arg	Glu	Gln	Arg	Arg	Arg	Ala	Val	Gly	Leu	Ala	Ala	
	225					230					235					240	
	Val	Val	Leu	Leu	Ala	Phe	Val	Thr	Cys	Phe	Ala	Pro	Asn	Asn	Phe	Val	
					245					250					255		
35	Leu	Leu	Ala	His	Ile	Val	Ser	Arg	Leu	Phe	Tyr	Gly	Lys	Ser	Tyr	Tyr	
				260					265					270			

09675076.060604

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300
 5 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335
 10 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350
 Gln Arg Gln Glu Ser Val Phe
 355

(30) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGAGCGTC CCTGGGAGGA CAGCCCAGGC CCGGAGGGGG CAGCTGAGGG CTCGCCTGTG 60
 CCAGTCGCCG CCGGGGCGCG CTCCGGTGCC GCGGCGAGTG GCACAGGCTG GCAGCCATGG 120
 GCTGAGTGCC CGGGACCCAA GGGGAGGGGG CAACTGCTGG CGACCGCCGG CCCTTTGCGT 180
 CGCTGGCCCG CCCCCTCGCC TGCCAGCTCC AGCCCCGCCC CCGGAGCGGC GTCCGCTCAC 240
 25 TCGGTTCAAG GCAGCGCGAC TGCGGGTGGC GCACGACCAG GGCGCAGACC TTGGGGCGCG 300
 CGGCCCATGG AGTCGGGGCT GCTGCGGCCG GCGCCGGTGA GCGAGGTCAT CGTCCTGCAT 360
 TACAACTACA CCGGCAAGCT CCGCGGTGCG AGCTACCAGC CCGGTGCCCG CCTGCGCGCC 420
 GACGCCGTGG TGTGCCTGGC GGTGTGCGCC TTCATCGTGC TAGAGAATCT AGCCGTGTTG 480
 TTGGTGCTCG GACGCCACCC GCGCTTCCAC GCTCCCATGT TCCTGCTCCT GGGCAGCCTC 540
 30 ACGTTGTCTGG ATCTGCTGGC AGGCGCCGCC TACGCCGCCA ACATCCTACT GTCGGGGCCG 600
 CTCACGCTGA AACTGTCCCC CGCGCTCTGG TTCGCACGGG AGGGAGGCGT CTTCTGTGGCA 660
 CTCACTGCGT CCGTGCTGAG CCTCCTGGCC ATCGCGCTGG AGCGCAGCCT CACCATGGCG 720

09875076 060601

CGCAGGGGGC CCGCGCCCGT CTCCAGTCGG GGGCGCACGC TGGCGATGGC AGCCGCGGCC 780
 TGGGGCGTGT CGCTGCTCCT CGGGCTCCTG CCAGCGCTGG GCTGGAATTG CCTGGGTCCG 840
 CTGGACGCTT GCTCCACTGT CTTGCCGCTC TACGCCAAGG CCTACGTGCT CTTCTGCGTG 900
 CTCGCCTTCG TGGGCATCCT GGCCGCGATC TGTGCACTCT ACGCGCGCAT CTACTGCCAG 960
 5 GTACGCGCCA ACGCGCGGCG CCTGCCGGCA CGGCCCCGGA CTGCGGGGAC CACCTCGACC1020
 CGGGCGCGTC GCAAGCCGCG CTCTCTGGCC TTGCTGCGCA CGCTCAGCGT GGTGCTCCTG1080
 GCCTTTGTGG CATGTTGGGG CCCCTCTTC CTGCTGCTGT TGCTCGACGT GCGTGCCCG1140
 GCGCGCACCT GTCCTGTACT CCTGCAGGCC GATCCCTTCC TGGGACTGGC CATGGCCAAC1200
 TCACTTCTGA ACCCCATCAT CTACACGCTC ACCAACC GCG 1260
 10 CGCCTGGTCT GCTGCGGACG CCACTCCTGC GGCAGAGACC CGAGTGGCTC CCAGCAGTCG1320
 GCGAGCGCGG CTGAGGCTTC CGGGGGCCTG CGCCGCTGCC TGCCCCCGGG CCTTGATGGG1380
 AGCTTCAGCG GCTCGGAGCG CTCATCGCCC CAGCGCGACG GGCTGGACAC CAGCGGCTCC1440
 ACAGGCAGCC CCGGTGCACC CACAGCCGCC CGGACTCTGG TATCAGAACC GGCTGCAGAC1500
 TGA 1503

15 (31) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
 1 5 10 15
 25 Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
 20 25 30
 Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
 35 40 45
 30 Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
 50 55 60
 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
 65 70 75 80

09875076-060601

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg
 85 90 95
 Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro
 100 105 110
 5 Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg
 115 120 125
 Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val
 130 135 140
 10 Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu
 145 150 155 160
 Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu
 165 170 175
 Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala
 180 185 190
 15 Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala
 195 200 205
 Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser
 210 215 220
 20 Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala
 225 230 235 240
 Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met
 245 250 255
 Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala
 260 265 270
 25 Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu
 275 280 285
 Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val
 290 295 300
 30 Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln
 305 310 315 320
 Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly
 325 330 335
 Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu
 340 345 350
 35 Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro
 355 360 365
 Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys

09875076-050501
 T09090" 9205/860

370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn
385 390 395 400

5 Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg
405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg
420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly
435 440 445

10 Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly
450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser
465 470 475 480

15 Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu
485 490 495

Pro Ala Ala Asp
500

(32) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGGAACA CCAGTCTGTG CACCAGAGAC 60
TACAAAATCA CCCAGGTCCT CTTCCCACTG CTCTACACTG TCCTGTTTTT TGTGGGACTT 120
ATCACAAATG GCCTGGCGAT GAGGATTTTC TTTCAAATCC GGAGTAAATC AAACCTTTATT 180
ATTTTTCTTA AGAACACAGT CATTTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAAA 240
30 ATTCTTAGTG ATGCCAACT GGGAACAGGA CCACTGAGAA CTTTTGTGTG TCAAGTTACC 300
TCCGTCATAT TTTATTTTAC AATGTATATC AGTATTTTAT TCCTGGGACT GATAACTATC 360
GATCGCTACC AGAAGACCAC CAGGCCATTT AAAACATCCA ACCCCAAAAA TCTCTTGGGG 420
GCTAAGATTG TCTCTGTTGT CATCTGGGCA TTCATGTTCT TACTCTCTTT GCCTAACATG 480

090505.000001

ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTTT CCTTAAATCA 540
 GAGTTCGGTC TAGTCTGGCA TGAAATAGTA AATTACATCT GTCAAGTCAT TTTCTGGATT 600
 AATTTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTCATAC 660
 GTAAGAACGA GGGGTGTAGG TAAAGTCCCC AGGAAAAAGG TGAACGTCAA AGTTTTCATT 720
 5 ATCATTGCTG TATTCTTTAT TTGTTTGTGTT CCTTTCCATT TTGCCCGAAT TCCTTACACC 780
 CTGAGCCAAA CCCGGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA 840
 GAGAGCACTC TGTGGTTAAC TTCCTTAAAT GCATGCCTGG ATCCGTTTAT CTATTTTTC 900
 CTTTGCAAGT CCTTCAGAAA TTCCTTGATA AGTATGCTGA AGTGCCCCAA TTCTGCAACA 960
 TCTCTGTCCC AGGACAATAG GAAAAAAGAA CAGGATGGTG GTGACCCAAA TGAAGAGACT1020
 10 CCAATGTAA 1029

(33) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

20 Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
 1 5 10 15
 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 20 25 30
 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
 35 40 45
 25 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 50 55 60
 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 65 70 75 80
 30 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 85 90 95
 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 100 105 110
 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg

09875076-050501

115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140

5 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
180 185 190

10 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
210 215 220

15 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
260 265 270

20 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
290 295 300

25 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
325 330 335

Asn Glu Glu Thr Pro Met
340

30 (34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09675076.060601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGCGG 60
 GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG GGCTGCCTGG CAACGGCTTC 120
 GTGGTGTGGA GCTTGGCGGG CTGGCGGCCT GCACGGGGGC GACCGCTGGC GGCCACGCTT 180
 5 GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGCTGC TCACGCCGCT CTTTGTGGCC 240
 TTCCTGACCC GGCAGGCCTG GCCGCTGGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG 300
 TGC GCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT GCAGCGCTGC 360
 CTCGCAGTCA CCCGCCCCCTT CCTGGCGCCT CGGCTGCGCA GCCCGGCCCT GGCCCGCCGC 420
 CTGCTGCTGG CGGTCTGGCT GGCCGCCCTG TTGCTCGCCG TCCCGGCCGC CGTCTACCGC 480
 10 CACCTGTGGA GGGACCGCGT ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC 540
 CACCTGAGCC TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC 600
 TACAGCGTGA CGCTGGCACG GCTGCGGGGC GCCCGCTGGG GCTCCGGGCG GCACGGGGCG 660
 CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG GCTTGCTCTG GGCCCCCTAC 720
 CACGCAGTCA ACCTTCTGCA GGCGGTCGCA GCGCTGGCTC CACCGGAAGG GGCCTTGGCG 780
 15 AAGCTGGGCG GAGCCGGCCA GCGGGCGCGA GCGGGAATA CGGCCTTGGC CTTCTTCAGT 840
 TCTAGCGTCA ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CCGGGCAGGT 900
 CCCCCTTTCC TCACGCGGCT CTTCAAGGC TCTGGGGAGG CCCGAGGGGG CGGCCGCTCT 960
 AGGGAAGGGA CCATGGAGCT CCGAACTACC CCTCAGCTGA AAGTGGTGGG GCAGGGCCGC1020
 GGCAATGGAG ACCCGGGGGG TGGGATGGAG AAGGACGGTC CGGAATGGGA CCTTTGA 1077

20 (35) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp
 1 5 10 15
 30 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu

09875076-060601

	20	25	30
	Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp 35 40 45		
5	Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu 50 55 60		
	Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala 65 70 75 80		
	Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala 85 90 95		
10	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr 100 105 110		
	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu 115 120 125		
15	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala 130 135 140		
	Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg 145 150 155 160		
	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val 165 170 175		
20	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu 180 185 190		
	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu 195 200 205		
25	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg 210 215 220		
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr 225 230 235 240		
	His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu 245 250 255		
30	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly 260 265 270		
	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr 275 280 285		
35	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu 290 295 300		
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser 305 310 315 320		

09875076 " 060601
 109090" 92052860

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val
325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp
340 345 350

5 Gly Pro Glu Trp Asp Leu
355

(36) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

15 ATGCTGGGGA TCATGGCATG GAATGCAACT TGCAAAACT GGCTGGCAGC AGAGGCTGCC 60
CTGGAAAAGT ACTACCTTTC CATTTTTTAT GGGATTGAGT TCGTTGTGGG AGTCCTTGGA 120
AATACCATTG TTGTTTACGG CTACATCTTC TCTCTGAAGA ACTGGAACAG CAGTAATATT 180
TATCTCTTTA ACCTCTCTGT CTCTGACTTA GCTTTTCTGT GCACCCTCCC CATGCTGATA 240
AGGAGTTATG CCAATGGAAA CTGGATATAT GGAGACGTGC TCTGCATAAG CAACCGATAT 300
20 GTGCTTCATG CCAACCTCTA TACCAGCATT CTCTTTCTCA CTTTATCAG CATAGATCGA 360
TACTTGATAA TTAAGTATCC TTTCCGAGAA CACCTTCTGC AAAAGAAAGA GTTTGCTATT 420
TTAATCTCCT TGGCCATTTG GGTTTTAGTA ACCTTAGAGT TACTACCCAT ACTTCCCCTT 480
ATAAATCCTG TTATAACTGA CAATGGCACC ACCTGTAATG ATTTTGCAAG TTCTGGAGAC 540
CCCAACTACA ACCTCATTTA CAGCATGTGT CTAACACTGT TGGGGTTCCT TATTCTCTT 600
25 TTTGTGATGT GTTCTTTTTA TTACAAGATT GCTCTCTTCC TAAAGCAGAG GAATAGGCAG 660
GTTGCTACTG CTCTGCCCCCT TGAAAAGCCT CTCAACTTGG TCATCATGGC AGTGGTAATC 720
TTCTCTGTGC TTTTACACC CTATCACGTC ATGCGGAATG TGAGGATCGC TTCACGCCTG 780
GGGAGTTGGA AGCAGTATCA GTGCACTCAG GTCGTCATCA ACTCCTTTTA CATTGTGACA 840
CGGCCTTTGG CCTTTCTGAA CAGTGTCTATC AACCCTGTCT TCTATTTTCT TTTGGGAGAT 900
30 CACTTCAGGG ACATGCTGAT GAATCAACTG AGACACAAC TCAAATCCCT TACATCCTTT 960
AGCAGATGGG CTCATGAACT CCTACTTTCA TTCAGAGAAA AGTGA 1005

09875075-060601

(37) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
 1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
 20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
 35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
 50 55 60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
 65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
 85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
 100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
 115 120 125

Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
 130 135 140

Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
 145 150 155 160

Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
 165 170 175

Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
 180 185 190

Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
 195 200 205

Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
 210 215 220

T09090" 92057860

Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
 225 230 235 240
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
 245 250 255
 5 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
 260 265 270
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
 275 280 285
 10 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300
 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320
 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
 325 330

15 (38) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCAGGCGC TTAACATTAC CCCGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAACCTG 60
 ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG 120
 25 CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC 180
 TTTGGCAATG CTCTGGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC 240
 AACATCTTTA TCTGCTCCTT GGCGCTCAGT GACCTGTCTA TCACCTTCTT CTGCATTCCC 300
 GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG 360
 GTGCCATTTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT 420
 30 GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAATGA AGTGGCAATA CACCAACCGA 480
 AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG 540
 TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC 600
 TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC 660

T09090" 92052860

ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA 720
CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA 780
ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTGTCCATTA TGATGGTGAC AGTGGTGGCT 840
CTCTTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT 900
5 TTTGAAAAGG AATATGATGA TGTCACAATC AAGATGATTT TTGCTATCGT GCAAATTATT 960
GGATTTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTCAAA1020
AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA1080
AGGCATGGAA ATTCAGGAAT TACAATGATG CGGAAGAAAAG CAAAGTTTTC CCTCAGAGAG1140
AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG1200
10 TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA1260
CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTAA 1296

(39) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
1 5 10 15
Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
20 25 30
Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
25 35 40 45
Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
50 55 60
Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
65 70 75 80
30 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
85 90 95
Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu

	100	105	110
	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala 115	120	125
5	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His 130	135	140
	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg 145	150	155 160
	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val 165	170	175
10	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe 180	185	190
	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro 195	200	205
15	Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu 210	215	220
	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu 225	230	235 240
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile 245	250	255
20	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val 260	265	270
	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro 275	280	285
25	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu 290	295	300
	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile 305	310	315 320
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn 325	330	335
30	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val 340	345	350
	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr 355	360	365
35	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu 370	375	380
	Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu 385	390	395 400

09875076 "060601

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
420 425 430

5 (40) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTGTGTACAG CAGTTCGCAG AGTG

24

(41) INFORMATION FOR SEQ ID NO:40:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGTGCCAGG CAGAGCAGGT AGAC

24

(42) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGAATTCC TGCTTGCTCC CAGCTTGGCC C

31

(43) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGTGGATCCT GCTGTCAAAG GTCCCATTCG GG

32

10 (44) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCACAATGCT AGGTGTGGTC

20

20 (45) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGCATAGACA ATGGGATTAC AG

22

30 (46) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

09075076 "060604
T09090" 9/05/86

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACAATGCT AGGTGTGGTC TGGCTGGTGG CAGTCATCGT AGGATCACCC ATGTGGCACG 60
5 TGCAACAAC T GAGATCAAA TATGACTTCC TATATGAAAA GGAACACATC TGCTGCTTAG 120
AAGAGTGGAC CAGCCCTGTG CACCAGAAGA TCTACACCAC CTCATCCTT GTCATCCTCT 180
TCCTCCTGCC TCTTATGGTG ATGCTTATTC TGTACGTAAA ATTGGTTATG AACTTTGGAT 240
AAAGAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCCAA 300
AATAGCCAGG AAGAAGAAAC GAGCTGTCTAT TATGATGGTG ACAGTGGTGG CTCTCTTTGC 360
10 TGTGTGCTGG GCACCATTC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAA 420
GGAATATGAT GATGTCACAA TCAAGATGAT TTTTGCTATC GTGCAAATTA TTGGATTTTC 480
CAACTCCATC TGTAATCCCA TTGTCTATGC A 511

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGCTTAGAA GAGTGGACCA G 21

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

09895076-050504
T09090"92054860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTGTGCACCA GAAGATCTAC AC

22

(49) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAAGGATGAA GGTGGTGTAG A

21

(50) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGTAGATCT TCTGGTGCAC AGG

23

(51) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAATGCAGG TCATAGTGAG C

21

(52) INFORMATION FOR SEQ ID NO:51:

09875076-060604

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

10 TGGAGCATGG TGACGGAAT GCAGAAG

27

(53) INFORMATION FOR SEQ ID NO:52:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20 GTGATGAGCA GGTCACTGAG CGCCAAG

27

(54) INFORMATION FOR SEQ ID NO:53:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

30 GCAATGCAGG CGCTTAACAT TAC

23

(55) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTGGGTTACA ATCTGAAGGG CA

22

(56) INFORMATION FOR SEQ ID NO:55:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACTCCGTGTC CAGCAGGACT CTG

23

(57) INFORMATION FOR SEQ ID NO:56:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGCGTGTTC TGGACCCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:57:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CAGGCCTTGG ATTTAATGT CAGGGATGG

29

5 (59) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGAGAGTCAG CTCTGAAAGA ATTCAGG

27

15 (60) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGATGTGATG CCAGATACTA ATAGCAC

27

25 (61) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

09875076-060604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCTGATTCAT TTAGGTGAGA TTGAGAC

27

(62) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACAGGTACC TTGCCATCAA G

21

(63) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCACAATG CCAGTGATAA GG

22

(64) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGACTTCTT GTTCCTGGCA GCAGCGG

27

(65) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

10 AGACCAGCCA GGGCACGCTG AAGAGTG

27

(66) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

20 GATCAAGCTT CCATCCTACT GAAACCATGG TC

32

(67) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

30 GATCAGATCT CAGTTCCAAT ATTCACACCA CCGTC

35

(68) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:

T09090" 9/05/860

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGGTGTGCT CCATGGCATC CC

22

(69) INFORMATION FOR SEQ ID NO:68:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTAAGCCTCC CAGAACGAGA GG

22

(70) INFORMATION FOR SEQ ID NO:69:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGCGCAGGG TGAAGCCTGA GAGC

24

(71) INFORMATION FOR SEQ ID NO:70:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

26

CCAACACCAG CATCCATGGC ATCAAG

(75) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

27

GGAGAGTCAG CTCTGAAAGA ATTCAGG

TO 9050" 92052860

SEQUENCE LISTING

<110> Chen, Ruoping
Dang, Huong T.
Liaw, Chen W.
Lin, I-Lin

<120> Human Orphan G Protein Coupled Receptors

<130> AREN0050

<140> 09/471,044
<141> 1999-10-19

<150> 60/109,213
<151> 1998-11-20

<150> 60/120,416
<151> 1999-02-16

<150> 60,121,851
<151> 1999-02-26

<150> 60,123,946
<151> 1999-03-12

<150> 60/123,949
<151> 1999-03-12

<150> 60/136,436
<151> 1999-05-28

<150> 60/136,437
<151> 1999-05-28

<150> 60/136,439
<151> 1999-05-28

<150> 60/136,567
<151> 1999-05-28

<150> 60/137,127
<151> 1999-05-28

<150> 60/137,131
<151> 1999-05-28

<150> 60/141,448

09875076.0606001

<151> 1999-06-29

<150> 60/156,653

<151> 1999-09-29

<150> 60/156,633

<151> 1999-09-29

<150> 60/156,555

<151> 1999-09-29

<150> 60/156,634

<151> 1999-09-29

<150> 60/157,280

<151> 1999-10-01

<150> 60/157,294

<151> 1999-10-01

<150> 60/157,281

<151> 1999-10-01

<150> 60/157,293

<151> 1999-10-01

<150> 60/157,282

<151> 1999-10-01

<160> 74

<170> PatentIn Ver. 2.1

<210> 1

<211> 1260

<212> DNA

<213> Homo sapiens

<400> 1

```

atggtcttct cggcagtgtt gactgcgttc cataccggga catccaacac aacatttgtc 60
gtgtatgaaa acacctacat gaatattaca ctccctccac cattccagca tcttgacctc 120
agtccattgc ttagatatag ttttgaaacc atggctccca ctggtttgag ttctttgacc 180
gtgaatagta cagctgtgcc cacaacacca gcagcattta agagcctaaa cttgcctctt 240
cagatcacco tttctgctat aatgatattc attctgtttg tgtcttttct tgggaacttg 300
gttgtttgcc tcatggttta ccaaaaagct gccatgaggt ctgcaattaa catcctcctt 360
gccagcctag cttttgcaga catgttgctt gcagtgtga acatgccctt tgccctggta 420
actattctta ctaccgatg gatttttggg aaattcttct gtaggggtatc tgctatgttt 480
ttctggttat ttgtgataga aggagtagcc atcctgctca tcattagcat agataggttc 540

```

cttattatag tccagaggca ggataagcta aacccatata gagctaaggt tctgattgca 600
 gtttcttggg caacttcctt ttgtgtagct tttccttttag ccgtaggaaa ccccgacctg 660
 cagatacctt cccgagctcc ccagtgtgtg tttgggtaca caaccaatcc aggctaccag 720
 gcttatgtga ttttgatttc tctcatttct ttcttcatac ccttcctggg aatactgtac 780
 tcatttatgg gcatactcaa cacccttcgg cacaatgcct tgaggatcca tagctaccct 840
 gaaggtatat gcctcagcca ggccagcaaa ctgggtctca tgagtctgca gagaccttctc 900
 cagatgagca ttgacatggg ctttaaaaca cgtgccttca ccactatittt gattctcttt 960
 gctgtcttca ttgtctgctg ggccccattc accacttaca gccttgtggc aacattcagt 1020
 aagcactttt actatcagca caactttttt gagattagca cctggctact gtggctctgc 1080
 tacctcaagt ctgcattgaa tccgctgac tactactgga ggattaagaa attccatgat 1140
 gcttgctgg acatgatgcc taagtccttc aagtttttgc cgcagctccc tggtcacaca 1200
 aagcgacgga tacgtcctag tgctgtctat gtgtgtgggg aacatcggac ggtggtgtga 1260

<210> 2

<211> 419

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
 1 5 10 15

Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro
 20 25 30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
 35 40 45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
 50 55 60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
 65 70 75 80

Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
 85 90 95

Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
 100 105 110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
 115 120 125

Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
 130 135 140

Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe

145		150		155		160
Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser						
	165		170		175	
Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro						
	180		185		190	
Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys						
	195		200		205	
Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser						
	210		215		220	
Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln						
	225		230		235	240
Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu						
	245		250		255	
Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn						
	260		265		270	
Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala						
	275		280		285	
Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile						
	290		295		300	
Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe						
	305		310		315	320
Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val						
	325		330		335	
Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile						
	340		345		350	
Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro						
	355		360		365	
Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp						
	370		375		380	
Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr						
	385		390		395	400
Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg						

09675076-060601

Thr Val Val

<210> 3

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 3

```

atgttagcca acagctcctc aaccaacagt tctgttctcc cgtgtcctga ctaccgacct 60
accacccgcc tgcacttggt ggtctacagc ttggtgctgg ctgccgggct cccctcaac 120
gcgctagccc tctgggtctt cctgcgcgcg ctgcgcgtgc actcgggtgt gagcgtgtac 180
atgtgtaacc tggcggccag cgacctgtct ttcacctctt cgtgcccgt tcgtctctcc 240
tactacgcac tgcaccactg gcccttcccc gacctcctgt gccagacgac gggcgccatc 300
ttccagatga acatgtacgg cagctgcata ttctgatgc tcatcaacgt ggaccgctac 360
gccgccatcg tgcacccgct gcgactgcgc cacctgcggc ggcccgcgt ggcgcggctg 420
ctctgectgg gcgtgtgggc gctcatcctg gtgtttgcgc tgcccgcgc ccgcgtgcac 480
aggccctcgc gttgccgcta ccgggacctc gaggtgcgc tatgcttcga gagcttcacg 540
gacgagctgt ggaaaggcag gctgctgccc ctctgtctgc tggccgaggc gctgggcttc 600
ctgctgcccc tggcggcggt ggtctactcg tgggcccag tcttctggac gctggcgcgc 660
cccgacgcca cgcagagcca gcggcgcgcg aagaccgtgc gctcctgct ggctaacctc 720
gtcatcttcc tgctgtgctt cgtgccctac aacagcacgc tggcgggtcta cgggctgctg 780
cggagcaagc tgggtggcgc cagcgtgcct gcccgcgatc gcgtgcgcgc ggtgctgatg 840
gtgatggtgc tgctggccgg cgccaactgc gtgctggacc cgtggtgta ctactttagc 900
gccgagggct tccgcaacac cctgcgcggc ctgggcactc cgcaccgggc caggacctcg 960
gccaccaacg ggacgcgggc ggcgctcgcg caatccgaaa ggtccgccgt caccaccgac 1020
gccaccaggc cggatgccgc cagtcagggg ctgctccgac cctccgactc ccactctctg 1080
tcttccttca cacagtgtcc ccaggattcc gccctctga 1119

```

<210> 4

<211> 372

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro
  1                      5                      10                      15

```

```

Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val
      20                      25                      30

```

```

Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
      35                      40                      45

```


Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
 305 310 315 320

Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
 325 330 335

Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
 340 345 350

Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
 355 360 365

Asp Ser Ala Leu
 370

<210> 5
 <211> 1107
 <212> DNA
 <213> Homo sapiens

<400> 5
 atggccaact ccacaggggt gaacgcctca gaagtcgcag gctcgttggg gttgatcctg 60
 gcagctgtcg tggaggtggg ggcactgctg ggcaacggcg cgctgctggt cgtgggtgctg 120
 cgcacgcggg gactgcgcga cgcgctctac ctggcgcacc tgtgcgtcgt ggacctgctg 180
 gcggcgcgct ccacatgccc gctgggcctg ctggcgcgac cgccgcccgg gctgggcgcg 240
 gtgcgcctgg gcccgcgccc atgcccgcgc gctcgtcttc tctccgcgc tctgctgcg 300
 gcctgcacgc tcgggggtgg cgcacttggc ctggcacgct accgcctcat cgtgcacccg 360
 ctgcggccag gctcgcggcc gccgcctgtg ctgctgctca ccgccgtgtg ggccgcggcg 420
 ggactgctgg gcgcgctctc cctgctcggc ccgccgccc caccgcccc tgctcctgct 480
 cgctgctcgg tcttggtgg gggcctcgg cccttcgggc cgctctgggc cctgctggcc 540
 ttcgcgctgc ccgcctcct gctgctcggc gcctacggcg gcatcttctg ggtggcgcg 600
 cgcgctgccc tgaggcccc acggcggcg cgcggtccc gactccgctc ggactctctg 660
 gatagccgcc ttccatctt gccgcgctc cggcctcgcc tgcccgggg caaggcggcc 720
 ctggccccag cgctggccgt gggccaattt gcagcctgct ggctgcctta tggctgcgcg 780
 tgcctggcg ccgcagcgcg ggccgcggaa gccgaagcg ctgtcacctg ggtcgccctac 840
 tcggccttcg cggtcacc cttcctgtac gggctgctgc agcgccccgt gcgcttggca 900
 ctgggcccgc tctctcgccg tgcaactgct ggacctgtgc gggcctgcac tccgcaagcc 960
 tggcaccgc gggcactctt gcaatgcctc cagagacccc cagagggccc tgccgtaggc 1020
 ccttctgagg ctccagaaca gacccccgag ttggcaggag ggcggagccc cgcataccag 1080
 gggccacctg agagttctct ctcctga 1107

<210> 6
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu
1 5 10 15

Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn
20 25 30

Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
35 40 45

Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
50 55 60

Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
65 70 75 80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
85 90 95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
100 105 110

Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
115 120 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
130 135 140

Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
145 150 155 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
165 170 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Leu Gly Ala Tyr
180 185 190

Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
210 215 220

Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro
245 250 255

Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu
 260 265 270

Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe
 275 280 285

Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu
 290 295 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala
 305 310 315 320

Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly
 325 330 335

Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala
 340 345 350

Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser
 355 360 365

<210> 7

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 7

atggaatcat ctttctcatt tggagtgate cttgctgtcc tggcctccct catcattgct 60
 actaacacac tagtggtgt ggctgtgctg ctgttgatcc acaagaatga tgggtgtcagt 120
 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttggtgtggc catctctggc 180
 ctactcacag accagctctc cagcccttct cggccacac agaagaccct gtgcagcctg 240
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacgggcat gctgatcacc 300
 tttgacaggc accttgccat caagcagccc ttccgctact tgaagatcat gagtggggtc 360
 gtggccgggg cctgcattgc cgggctgtgg ttagtgtctt acctcattgg cttcctccca 420
 ctcggaatcc ccatgttcca gcagactgcc taaaaaggc agtgcagctt ctttgctgta 480
 tttcaccctc acttcgtgct gacctctcc tgcgttggct tcttcccagc catgctcctc 540
 tttgtcttct totactgcga catgctcaag attgcttcca tgcacagcca gcagattcga 600
 aagatggaac atgcaggagc catggctgga gggtatcgat cccacaggac tcccagcgac 660
 ttcaaagctc tccgtactgt gtctgttctc attgggagct ttgctctatc ctggaccccc 720
 ttccttatca ctggcattgt gcagggtggc tgccaggagt gtcaccteta cctagtgtgtg 780
 gaacggtaac tgtggtgtgt cggcgtgggc aactccctgc tcaaccact catctatgcc 840
 tattggcaga aggaggtgag actgcagctc taccacatgg ccctaggagt gaagaagggtg 900
 ctacacctcat tctcctctt tctctcggcc aggaattgtg gccagagag gccacgggaa 960

agttcctgtc acatcgtcac tatctccagc tcagagtttg atggcctaa

1008

<210> 8

<211> 335

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
1 5 10 15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
20 25 30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50 55 60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85 90 95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145 150 155 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165 170 175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180 185 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
 325 330 335

<210> 9
 <211> 1413
 <212> DNA
 <213> Homo sapiens

<400> 9
 atggacacta ccatggaagc tgacctgggt gccactggcc acaggccccg cacagagctt 60
 gatgatgagg actcctaccc ccaaggtggc tgggacacgg tcttcctggt ggccctgctg 120
 ctccctgggc tgccagccaa tgggttgatg gcgtggctgg ccggtcccca ggcccgcat 180
 ggagctggca cgcgtctggc gctgctcctg ctacgcctgg ccctctctga cttcttggtc 240
 ctggcagcag cggccttcca gatcctagag atccggcatg ggggacactg gccgctgggg 300
 acagctgcct gccgcttcta ctacttcta tggggcgtgt cctactcctc cggcctcttc 360
 ctgctggccg ccctcagcct cgaccgctgc ctgctggcgc tgtgccaca ctggtaccct 420
 gggcaccgcc cagtcgcctt gcccctctgg gtctgcgccg gtgtctgggt gctggccaca 480
 ctcttcagcg tgccctggct ggtcttcccc gaggtgccg tctggtggtg cgacctggtc 540
 atctgcctgg acttctggga cagcgaggag ctgtcgtgga ggatgctgga ggtcctgggg 600
 ggcttcctgc ctttctcctt gctgctcgtc tgccacgtgc tcacccaggc cacagcctgt 660
 cgcacctgcc accgccaaca gcagcccgca gcctgccggg gcttcgcccg tgtggccagg 720
 accattctgt cagcctatgt ggtcctgagg ctgccctacc agctggccca gctgctctac 780
 ctggccttcc tgtgggacgt ctactctggc tacctgctct gggaggccct ggtctactcc 840
 gactacctga tctactcaa cagctgcctc agccccttcc tctgcctcat ggccagtgcc 900
 gacctccgga ccctgctgcg ctccgtgctc tcgtccttcg cggcagctct ctgcgaggag 960
 cggccgggga gcttcacgcc cactgagcca cagaccagc tagattctga ggtccaact 1020

ctgccagagc cgatggcaga ggcccagtc aagatggatc ctgtggccca gcctcagggtg 1080
aacccacac tccagccacg atcggatccc acagctcagc cacagctgaa ccctacggcc 1140
cagccacagt cggatccac agcccagcca cagctgaacc tcatggccca gccacagtca 1200
gattctgtgg ccagccaca ggcagacact aacgtccaga cccctgcacc tgctgccagt 1260
tctgtgcca gtccctgtga tgaagcttcc ccaaccccat cctcgcatcc taccacaggg 1320
gcccttgagg acccagccac acctcctgcc totgaaggag aaagccccag cagcaccctg 1380
ccagaggcgg ccccgggcgc aggccccacg tga 1413

<210> 10

<211> 468

<212> PRT

<213> Homo sapiens

<400> 10

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro
1 5 10 15

Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly
35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr
50 55 60

Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe
65 70 75 80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His
85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly
100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp
115 120 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro
130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr
145 150 155 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp
165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser
 180 185 190
 Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu
 195 200 205
 Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln
 210 215 220
 Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile
 225 230 235 240
 Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu
 245 250 255
 Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp
 260 265 270
 Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu
 275 280 285
 Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu
 290 295 300
 Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro
 305 310 315 320
 Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly
 325 330 335
 Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro
 340 345 350
 Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
 355 360 365
 Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
 370 375 380
 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
 385 390 395 400
 Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
 405 410 415
 Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser
 420 425 430

09875076 060601
 T09090" 92090

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala
 435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly
 450 455 460

Ala Gly Pro Thr
 465

<210> 11
 <211> 1248
 <212> DNA
 <213> Homo sapiens

<400> 11
 atgtcaggga tggaaaaact tcagaatgct tcttggatct accagcagaa actagaagat 60
 ccattccaga aacacctgaa cagcaccgag gagtatctgg ccttctctctg cggacctcgg 120
 cgcagccact tcttctctccc cgtgtctgtg gtgtatgtgc caatttttgt ggtgggggtc 180
 attggcaatg tcttgggtgtg cctgggtgatt ctgcagcacc aggctatgaa gacgcccacc 240
 aactactacc tcttcagcct ggcggtctct gacctcctgg tctgtctctt tggaatgcc 300
 ctggaggtct atgagatgtg gcgcaactac cctttcttgt tcggggcccg gggctgtctac 360
 ttcaagacgg cctcttttga gaccgtgtgc ttgcctcca tcttcagcat caccaccgtc 420
 agcgtggagc gctacgtggc catctacac cgttcccg ccaaactgca gagcaccgg 480
 cgccggggccc tcaggatcct cggcatcgtc tggggcttct cgtgtctctt ctccctgcc 540
 aacaccagca tccatggcat caagtccac tacttcccca atgggtccct ggtcccaggt 600
 tcggccacct gtaaggatcat caagcccatg tggatctaca atttcatcat ccaggtcacc 660
 tcttctctat tctacctcct ccccatgact gtcactcagt tctctacta cctcatggca 720
 ctcagactaa agaaagacaa atctcttgag gcagatgaag ggaatgcaaa tattcaaaga 780
 ccttgacagaa aatcagtcaa caagatgctg tttgtcttgg tcttagtggt tgctatctgt 840
 tggggcccgct tccacattga ccgactcttc ttcagctttg tggaggagtg gagtgaatcc 900
 ctggctgctg tgttcaacct cgtccatgtg gtgtcagggt tcttcttcta cctgagctca 960
 gctgtcaacc ccattatcta taacctactg tctcgcgct tccaggcagc attccagaat 1020
 gtgatctctt ctttccacaa acagtggcac tcccagcatg accacagtt gccacctgcc 1080
 cagcggaaca tcttcttgac agaatgccac tttgtggagc tgaccgaaga tatagggtccc 1140
 caattcccat gtcagtcac catgcacaac tctcacctcc caacagccct ctctagttaa 1200
 cagatgtcaa gaacaaacta tcaaagcttc cactttaaca aaacctga 1248

<210> 12
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
 1 5 10 15

Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
 20 25 30
 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
 35 40 45
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
 50 55 60
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
 65 70 75 80
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
 85 90 95
 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
 100 105 110
 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
 115 120 125
 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
 130 135 140
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
 145 150 155 160
 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
 165 170 175
 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
 180 185 190
 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
 195 200 205
 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
 210 215 220
 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
 225 230 235 240
 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
 245 250 255
 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
 260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
 275 280 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val
 290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
 305 310 315 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
 325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
 340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
 355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
 370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
 385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
 405 410 415

<210> 13
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<400> 13
 atgccagata ctaatagcac aatcaattta tcactaagca ctcgtgttac tttagcattt 60
 tttatgtcct tagtagcttt tgctataatg ctaggaaatg ctttggtcat tttagctttt 120
 gtggtggaca aaaaccttag acatcgaagt agttattttt ttcttaactt ggccatctct 180
 gacttccttg tgggtgtgat ctccattcct ttgtacatcc ctcacacgct gttcgaatgg 240
 gatcttgtaa aggaaatctg tgtatttttg ctactactg actatctgtt atgtacagca 300
 tctgtatata acattgtcct catcagctat gatcgatacc tgtcagtctc aaatgctgtg 360
 tcttatagaa ctcaacatac tggggctctg aagattgtta ctctgatggg ggccgtttgg 420
 gtgctggcct tcttagtgaa tgggccaatg attctagttt cagagtcttg gaaggatgaa 480
 ggtagtgaat gtgaacctgg atttttttcg gaatggtaca tccttgccat cacatcattc 540
 ttggaattcg tgatcccagt catcttagtc gcttatttca acatgaatat ttattggagc 600
 ctgtggaagc gtgatcatct cagtaggtgc caaagccatc ctggactgac tgctgtctct 660
 tccaacatct gtggacactc attcagaggt agactatctt caaggagatc tctttctgca 720
 tcgacagaag ttctgtcatc ctttcattca gagagacaga ggagaaagag tagtctcatg 780
 ttttctcaa gaaccaagat gaatagcaat acaattgctt ccaaaatggg ttccttctcc 840

caatcagatt ctgtagctct tcaccaaagg gaacatgttg aactgcttag agccaggaga 900
 ttagccaagt cactggccat tctcttaggg gtttttgctg tttgctgggc tccatattct 960
 ctgttcacaa ttgtcctttc attttattcc tcagcaacag gtcctaaatc agtttggtat 1020
 agaattgcat ttgggttca gtggttcaat tcctttgtca atcctctttt gtatccattg 1080
 tgtcacaagc gctttcaaaa ggctttcttg aaaatatatt gtataaaaaa gcaacctcta 1140
 ccatcacaac acagtcggtc agtatcttct taa 1173

<210> 14
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
 1 5 10 15
 Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
 20 25 30
 Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
 35 40 45
 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
 50 55 60
 Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
 65 70 75 80
 Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
 85 90 95
 Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
 100 105 110
 Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
 115 120 125
 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
 130 135 140
 Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
 145 150 155 160
 Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
 165 170 175
 Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr

180	185	190
Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser		
195	200	205
Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys		
210	215	220
Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala		
225	230	235 240
Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys		
	245	250 255
Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile		
	260	265 270
Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His		
	275	280 285
Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser		
	290	295 300
Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser		
305	310	315 320
Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys		
	325	330 335
Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe		
	340	345 350
Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala		
	355	360 365
Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His		
	370	375 380
Ser Arg Ser Val Ser Ser		
385		390

<210> 15
 <211> 1128
 <212> DNA
 <213> Homo sapiens

 <400> 15

```

atggcgaacg cgagcgagcc ggggtggcagc ggcgggcgcg aggcggccgc cctgggcctc 60
aagctggcca cgctcagcct gctgctgtgc gtgagcctag cgggcaacgt gctgttcgcg 120
ctgctgatcg tgcgggagcg cagcctgcac cgcgccccgt actacctgct gctcgacctg 180
tgcttgcccg acgggctgcg cgcgctcgcc tgctcccgcg ccgtcatgct ggcggcgcgg 240
cgtgcggcgg ccgcggcggg ggcgccgccc ggcgcgctgg gctgcaagct gctcgccctc 300
ctggccgcgc tcttctgttt ccacgcgcgc ttctgtgtgc tgggcgtggg cgtcaccgcg 360
tacctggcca tcgcgcacca ccgcttctat gcagagcgcc tggccggctg gccgtgcgcc 420
gccatgctgg tgtgcgcgcg ctgggcgctg gcgctggccg cggccttccc gccagtgtg 480
gacggcggtg gcgacgacga ggacgcgcgg tgcgccttg agcagcggcc cgacggcgcc 540
cccggcgcgc tgggcttctt gctgctgtgc gccgtggtgg tgggcgccac gcacctcgtc 600
tacctcgccc tgctcttctt catccacgac cgcgcgaaga tgcggcccg cgcctggtg 660
cccgcggtca gccacgactg gaccttccac ggcccgggcg ccaccggcca ggcggcgcgc 720
aactggacgg cgggcttcgg ccgcgggccc acgcgcgcgg cgcttgtggg catccggccc 780
gcagggcggg gccgcggcgc gcgcgcctc ctgctgtgga aagaattcaa gacggagaag 840
aggctgtgca agatgttcta cgcggtcacg ctgctcttcc tgctcctctg gggggccctac 900
gtcgtggcca gctacctgcg ggtcctggtg cggcccgcg ccgtccccc gccctacctg 960
acggcctcgc tgtggctgac cttcgcgcag gccggcatca acccgcgtgt gtgcttctc 1020
ttcaacaggg agctgagggg ctgcttcagg gccagttcc cctgctgcca gagcccccg 1080
accaccaggg cgaccatcc ctgcgacctg aaaggcattg gtttatga 1128

```

```

<210> 16
<211> 375
<212> PRT
<213> Homo sapiens

```

```

<400> 16
Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Glu Ala Ala
  1             5             10             15

Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
      20             25             30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
      35             40             45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
      50             55             60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
      65             70             75             80

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
      85             90             95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
      100            105            110

```

Leu	Leu	Gly	Val	Gly	Val	Thr	Arg	Tyr	Leu	Ala	Ile	Ala	His	His	Arg	115	120	125	
Phe	Tyr	Ala	Glu	Arg	Leu	Ala	Gly	Trp	Pro	Cys	Ala	Ala	Met	Leu	Val	130	135	140	
Cys	Ala	Ala	Trp	Ala	Leu	Ala	Leu	Ala	Ala	Ala	Phe	Pro	Pro	Val	Leu	145	150	155	160
Asp	Gly	Gly	Gly	Asp	Asp	Glu	Asp	Ala	Pro	Cys	Ala	Leu	Glu	Gln	Arg	165	170	175	
Pro	Asp	Gly	Ala	Pro	Gly	Ala	Leu	Gly	Phe	Leu	Leu	Leu	Leu	Ala	Val	180	185	190	
Val	Val	Gly	Ala	Thr	His	Leu	Val	Tyr	Leu	Arg	Leu	Leu	Phe	Phe	Ile	195	200	205	
His	Asp	Arg	Arg	Lys	Met	Arg	Pro	Ala	Arg	Leu	Val	Pro	Ala	Val	Ser	210	215	220	
His	Asp	Trp	Thr	Phe	His	Gly	Pro	Gly	Ala	Thr	Gly	Gln	Ala	Ala	Ala	225	230	235	240
Asn	Trp	Thr	Ala	Gly	Phe	Gly	Arg	Gly	Pro	Thr	Pro	Pro	Ala	Leu	Val	245	250	255	
Gly	Ile	Arg	Pro	Ala	Gly	Pro	Gly	Arg	Gly	Ala	Arg	Arg	Leu	Leu	Val	260	265	270	
Leu	Glu	Glu	Phe	Lys	Thr	Glu	Lys	Arg	Leu	Cys	Lys	Met	Phe	Tyr	Ala	275	280	285	
Val	Thr	Leu	Leu	Phe	Leu	Leu	Leu	Trp	Gly	Pro	Tyr	Val	Val	Ala	Ser	290	295	300	
Tyr	Leu	Arg	Val	Leu	Val	Arg	Pro	Gly	Ala	Val	Pro	Gln	Ala	Tyr	Leu	305	310	315	320
Thr	Ala	Ser	Val	Trp	Leu	Thr	Phe	Ala	Gln	Ala	Gly	Ile	Asn	Pro	Val	325	330	335	
Val	Cys	Phe	Leu	Phe	Asn	Arg	Glu	Leu	Arg	Asp	Cys	Phe	Arg	Ala	Gln	340	345	350	
Phe	Pro	Cys	Cys	Gln	Ser	Pro	Arg	Thr	Thr	Gln	Ala	Thr	His	Pro	Cys	355	360	365	

Asp Leu Lys Gly Ile Gly Leu
370 375

<210> 17
<211> 1002
<212> DNA
<213> Homo sapiens

<400> 17
atgaacacca cagtgatgca aggcttcaac agatctgagc ggtgccccag agacactcgg 60
atagtacagc tggattccc agccctctac acagtggttt tcttgaccgg catcctgctg 120
aatacttttg ctctgtgggt gtttggtcac atccccagct cctccacctt catcatctac 180
ctcaaaaaca ctttggtggc cgacttgata atgacactca tgcttccttt caaaatcctc 240
tctgactcac acctggcacc ctggcagctc agagcttttg tgtgtcgttt ttcttcggtg 300
atattttatg agaccatgta tgtgggcata gtgctgtag ggctcatagc ctttgacaga 360
ttcctcaaga tcatcagacc tttagaaaat atttttctaa aaaaacctgt ttttgcaaaa 420
acggtctcaa tcttcatctg gttctttttg ttcttcatct ccttgccaaa tacgatcttg 480
agcaacaagg aagcaacacc atcgtctgtg aaaaagtgtg ctctcttaaa ggggcctctg 540
gggctgaaat ggcatacaat ggtaataaac atatgccagt ttattttctg gactgttttt 600
atcctaatac ttgtgtttta tgtggttatt gcaaaaaaag tatatgattc ttatagaaag 660
tcaaaaagta aggacagaaa aaacaacaaa aagctggaag gcaaagtatt tgttgtcgtg 720
gctgtcttct ttgtgtgttt tgctccattt cattttgcca gagttccata tactcacagt 780
caaaccaaca ataagactga ctgtagactg caaaatcaac tgttttattgc taaagaaaca 840
actctctttt tggcagcaac taacatttgt atggatccct taatatacat attcttatgt 900
aaaaaattca cagaaaagct accatgtatg caagggagaa agaccacagc atcaagccaa 960
gaaaatcata gcagtcagac agacaacata accttaggct ga 1002

<210> 18
<211> 333
<212> PRT
<213> Homo sapiens

<400> 18
Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1 5 10 15
Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20 25 30
Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35 40 45
Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60
Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu

65

70

75

80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly

09875076-060604

<210> 19
 <211> 1122
 <212> DNA
 <213> Homo sapiens

<400> 19
 atggccaaca ctaccggaga gcctgaggag gtgagcggcg ctctgtcccc accgtccgca 60
 tcagcttatg tgaagctggg actgctggga ctgattatgt gcgtgagcct ggcgggtaac 120
 gccatcttgt cctgctggg gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180
 ctgctggacc tgtgctggc cgatggcata cgctctgcg tctgcttccc ctttgtgctg 240
 gcttctgtgc gccacggctc ttcattggacc ttcagtgcac tcagctgcaa gattgtggcc 300
 tttatggccg tgctcttttg cttccatgcg gccttcatgc tgttctgcat cagcgtcacc 360
 cgctacatgg ccatcgccca ccaccgcttc tacgccaagc gcatgacact ctggacatgc 420
 gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt 480
 gacgtgggca cctacaagtt tattcgggag gaggaccagt gcatctttga gcatcgctac 540
 ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc 600
 catgctgtct acggcaagct gctcctcttc gagtatcgtc accgcaagat gaagccagtg 660
 cagatgggtc cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag 720
 gctgctgcca actggatcgc cggctttggc cgtggggcca tgccaccaac cctgctgggt 780
 atccggcaga atgggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt 840
 gaaaagcagc tgggccgcat gttctacgcg atcacactgc tctttctgct cctctgggtca 900
 ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gcccaccgc 960
 tacctggcca ctgctgtttg gatgagcttc gccaggtg ccgtcaaccc aattgtctgc 1020
 ttcctgctca acaaggacct caagaagtgc ctgaccactc acgccccctg ctggggcaca 1080
 ggaggtgccc cggctcccag agaaccctac tgtgtcatgt ga 1122

<210> 20
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
 1 5 10 15
 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30
 Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
 65 70 75 80
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140
 Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160
 Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175
 Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr
 340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365

Pro Tyr Cys Val Met
 370

<210> 21
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<400> 21
 atggcttttg aacagaacca gtcaacagat tattattatg aggaaaatga aatgaatggc 60
 acttatgact acagtcaata tgaattgac tgtatcaaag aagatgtcag agaatttgca 120
 aaagttttcc tccctgtatt cctcacaata gctttcgtca ttggacttgc aggcaattcc 180
 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
 ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcccttttg ggctgttaat 300
 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
 ctaaactttg tctctggaat gcagtttctg gcttgcacat gcatagacag atatgtggca 420
 gtaactaatg tccccagcca atcaggagtg ggaaaacat gctggatcat ctgtttctgt 480
 gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaatgac 540
 aatgctaggt gcattcccat tttccccgc tacctaggaa catcaatgaa agcattgatt 600
 caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgctac 660
 tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccctataa cattgtcaag 780
 ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
 atggacatcg ccatccaagt cacagaaagc attgcactct ttcacagctg cctcaaccca 900
 atcctttatg tttttatggg agcatcttcc aaaaactacg ttatgaaagt ggccaagaaa 960
 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttcccttttga ttctgagggt 1020
 cctacagagc caaccagtac ttttagcatt taa 1053

<210> 22
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
 1 5 10 15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile	20	25	30
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu	35	40	45
Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala	50	55	60
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile	65	70	75
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe	85	90	95
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys	100	105	110
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln	115	120	125
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val	130	135	140
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys	145	150	155
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr	165	170	175
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu	180	185	190
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly	195	200	205
Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala	210	215	220
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys	225	230	235
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr	245	250	255
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile	260	265	270

Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
 275 280 285

Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
 290 295 300

Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
 305 310 315 320

Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
 325 330 335

Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
 340 345 350

<210> 23
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<400> 23
 atgccaggaa acgccacccc agtgaccacc actgccccgt gggcctccct gggcctctcc 60
 gccaagacct gcaacaacgt gtccttcgaa gagagcagga tagtcctggt cgtggtgtac 120
 agcgcggtgt gcacgctggg ggtgccggcc aactgcctga ctgctggtgt ggcgctgctg 180
 caggctactgc agggcaacgt gctggccgtc tacctgctct gctggcact ctgcgaactg 240
 ctgtacacag gcacgctgcc actctgggtc atctatatcc gcaaccagca ccgctggacc 300
 ctaggcctgc tggcctcgaa ggtgaccgcc tacatcttct tctgcaacat ctacgtcagc 360
 atcctcttcc tgtgctgcat ctctgctgac cgcttcgtgg ccgtggtgta cgcgctggag 420
 agtcggggcc gccgcgcgcg gaggaccgcc atcctcatct ccgcctgcat cttcatcctc 480
 gtcgggatcg ttcactaccc ggtgttccag acggaagaca aggagacctg ctttgacatg 540
 ctgcagatgg acagcaggat tgccgggtac tactacgcca gggtcaccgt tggctttgcc 600
 atcctctctc ccatcatcgc cttcaccaac caccggattt tcaggagcat caagcagagc 660
 atgggcttaa gcgctgcccc gaaggccaag gtgaagcact cggccatcgc ggtggtgtc 720
 atcttcctag tctgcttcgc cccgtaccac ctggttctcc togtcaaagc cgctgccttt 780
 tcctactaca gaggagacag gaacgccatg tgcggcttgaggaggaggt gtacacagcc 840
 tctgtggtgt ttctgtgcct gtccacgggtg aacggcgtgg ctgaccccat tatctacgtg 900
 ctggccacgg accattcccc ccaagaagtg tccagaatcc ataaggggtg gaaagagtgg 960
 tccatgaaga cagacgtcac caggctcacc cacagcaggg acaccgagga gctgcagtcg 1020
 cccgtggccc ttgcagacca ctacaccttc tccaggcccc tgcacccacc agggtcacca 1080
 tgccctgcaa agaggctgat tgaggagtcc tgctga 1116

<210> 24
 <211> 371
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser
1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser
20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val
35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln
50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu
65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln
85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile
100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser
115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg
130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu
145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr
165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr
180 185 190

Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe
195 200 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser
210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val
225 230 235 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
245 250 255

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	10	16
Income	35000	15000	15000	70000
Health	0.8	0.2	0	1
Exercise	0.3	0.5	0	1
Stress	0.7	0.4	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Sleep	0.6	0.3	0	1
Diet	0.4	0.5	0	1
Work	0.5	0.5	0	1
Family	0.3	0.5	0	1
Friends	0.4	0.5	0	1
Hobbies	0.2	0.4	0	1
Travel	0.1	0.3	0	1
Religion	0.5	0.5	0	1
Politics	0.3	0.5	0	1
Environment	0.4	0.5	0	1
Technology	0.2	0.4	0	1
Art	0.1	0.3	0	1
Music	0.3	0.5	0	1
Gardening	0.2	0.4	0	1
Reading	0.4	0.5	0	1
Writing	0.1	0.3	0	1
Volunteering	0.2	0.4	0	1
Charitable	0.1	0.3	0	1
Philanthropy	0.1	0.3	0	1
Activism	0.2	0.4	0	1
Leadership	0.1	0.3	0	1
Entrepreneurship	0.1	0.3	0	1
Investment	0.1	0.3	0	1
Real Estate	0.1	0.3	0	1
Stocks	0.1	0.3	0	1
Bonds	0.1	0.3	0	1
Commodities	0.1	0.3	0	1
Cryptocurrency	0.1	0.3	0	1
Art Collection	0.1	0.3	0	1
Real Estate Collection	0.1	0.3	0	1
Stock Collection	0.1	0.3	0	1
Bond Collection	0.1	0.3	0	1
Commodity Collection	0.1	0.3	0	1
Cryptocurrency Collection	0.1	0.3	0	1
Art Collection Value	100000	50000	0	200000
Real Estate Collection Value	200000	100000	0	400000
Stock Collection Value	50000	25000	0	100000
Bond Collection Value	25000	12500	0	50000
Commodity Collection Value	12500	6250	0	25000
Cryptocurrency Collection Value	6250	3125	0	12500

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	45000	15000	20000	80000
Health	0.8	0.4	0	1
Exercise	0.3	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.4	0	1
Diet	0.5	0.5	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Family Size	2.5	1.5	1	6
Work Hours	40	10	20	60
Job Satisfaction	0.6	0.5	0	1
Life Satisfaction	0.7	0.4	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	16
Income	35000	15000	15000	70000
Health	0.8	0.4	0	1
Exercise	0.3	0.5	0	1
Stress	0.6	0.5	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Sleep	0.7	0.4	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.4	0	1
Family	0.6	0.5	0	1
Friends	0.7	0.4	0	1
Hobbies	0.5	0.5	0	1
Travel	0.4	0.5	0	1
Volunteering	0.3	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.4	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.3	0.5	0	1
Fishing	0.2	0.4	0	1
Reading	0.6	0.5	0	1
Writing	0.3	0.5	0	1
Learning	0.4	0.5	0	1
Teaching	0.2	0.4	0	1
Coaching	0.1	0.3	0	1
Consulting	0.3	0.5	0	1
Entrepreneurship	0.2	0.4	0	1
Investment	0.1	0.3	0	1
Real Estate	0.2	0.4	0	1
Technology	0.3	0.5	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.3	0.5	0	1
Mathematics	0.2	0.4	0	1
Physics	0.1	0.3	0	1
Chemistry	0.1	0.3	0	1
Biology	0.2	0.4	0	1
Medicine	0.1	0.3	0	1
Law	0.1	0.3	0	1
Business	0.2	0.4	0	1
Engineering	0.1	0.3	0	1
Architecture	0.1	0.3	0	1
Design	0.2	0.4	0	1
Art History	0.1	0.3	0	1
Music History	0.1	0.3	0	1
Science History	0.1	0.3	0	1
History of Art	0.1	0.3	0	1
History of Music	0.1	0.3	0	1
History of Science	0.1	0.3	0	1
History of Medicine	0.1	0.3	0	1
History of Law	0.1	0.3	0	1
History of Business	0.1	0.3	0	1
History of Engineering	0.1	0.3	0	1
History of Architecture	0.1	0.3	0	1
History of Design	0.1	0.3	0	1
History of Art History	0.1	0.3	0	1
History of Music History	0.1	0.3	0	1
History of Science History	0.1	0.3	0	1
History of Medicine History	0.1	0.3	0	1
History of Law History	0.1	0.3	0	1
History of Business History	0.1	0.3	0	1
History of Engineering History	0.1	0.3	0	1
History of Architecture History	0.1	0.3	0	1
History of Design History	0.1	0.3	0	1
History of Art History History	0.1	0.3	0	1
History of Music History History	0.1	0.3	0	1
History of Science History History	0.1	0.3	0	1
History of Medicine History History	0.1	0.3	0	1
History of Law History History	0.1	0.3	0	1
History of Business History History	0.1	0.3	0	1
History of Engineering History History	0.1	0.3	0	1
History of Architecture History History	0.1	0.3	0	1
History of Design History History	0.1	0.3	0	1
History of Art History History History	0.1	0.3	0	1
History of Music History History History	0.1	0.3	0	1
History of Science History History History	0.1	0.3	0	1
History of Medicine History History History	0.1	0.3	0	1
History of Law History History History	0.1	0.3	0	1
History of Business History History History	0.1	0.3	0	1
History of Engineering History History History	0.			

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.6	0.5	0	1
Quality of Life	0.7	0.5	0	1
Overall Health	0.8	0.4	0	1
Physical Health	0.9	0.3	0	1
Mental Health	0.7	0.5	0	1
Social Health	0.6	0.5	0	1
Emotional Health	0.5	0.5	0	1
Behavioral Health	0.4	0.5	0	1
Environmental Health	0.3	0.5	0	1
Occupational Health	0.2	0.4	0	1
Financial Health	0.1	0.3	0	1
Family Health	0.0	0.2	0	1
Community Health	0.0	0.1	0	1
National Health	0.0	0.0	0	1
Global Health	0.0	0.0	0	1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	16
Income	3500	1500	1000	8000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Exercise	0.2	0.4	0	1
Stress	0.6	0.5	0	1
Depression	0.4	0.5	0	1
Loneliness	0.5	0.5	0	1
Life Satisfaction	0.7	0.4	0	1
Quality of Life	0.8	0.3	0	1
Overall Health	0.9	0.2	0	1

ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatccttt tgtctgcatt 1020
 ttctcaaaca gggagctgag gcgctgtttc agcacaaccc ttctttactg cagaaaaatcc 1080
 aggttaccaa gggaacctta ctgtgttata tga 1113

<210> 26
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30
 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80
 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125
 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175
 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190
 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe

195 200 205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
210 215 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
225 230 235 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
245 250 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
260 265 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
275 280 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
290 295 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
305 310 315 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
325 330 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
355 360 365

Val Ile
370

<210> 27
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 27
atgcaggtcc cgaacagcac cggcccggac aacgcgacgc tgcagatgct gcggaacccg 60
gcgatcgcgg tggccttgcc cgtggtgtac tcgctggtgg cggcggtcag catcccgggc 120
aacctcttct ctctgtgggt gctgtgccgg cgcattggggc ccagatcccc gtcggtcata 180
ttcatgatca acctgagcgt cacggacctg atgctggcca gcgtgttgcc ttccaaatc 240
tactaccatt gcaaccgcca cactgggta ttcgggggtgc tgctttgcaa cgtggtgacc 300
gtggcctttt acgcaaacat gtattccagc atcctcacca tgacctgtat cagcgtggag 360

cgcttcctgg gggtcctgta cccgctcagc tccaagcgct ggcgccgccc tcgttaacgog 420
 gtggccgogt gtgcagggac ctggctgctg ctctgaccg ccctgtgccc gctggcgogc 480
 accgatctca cctaccgggt gcacgcctg ggcacatca cctgcttcga cgtcctcaag 540
 tggacgatgc tccccagcgt ggccatgtgg gccgtgttcc tcttcacat cttcatcctg 600
 ctgttcctca tcccgcttct gatcacctg gcttggtaca cggccacat cctcaagctg 660
 ttgcgcacgg aggaggcgca cggccgggag cagcgaggc gcgcggtggg cctggccgog 720
 gtggtcttgc tggcctttgt cacctgcttc gcccacaaca acttcgtgct cctggcgogc 780
 atcgtgagcc gcctgttcta cggcaagagc tactaccagc tgtacaagct cacgctgtgt 840
 ctacgtgcc tcaacaactg tctggaccog tttgtttatt actttgcgtc ccgggaattc 900
 cagctgcgcc tgcgggaata tttgggctgc cgcgggtgc ccagagacac cctggacacg 960
 cgccgcgaga gcctcttctc cgccaggacc acgtccgtgc gctccgaggc cgggtgcgogc 1020
 cctgaaggga tggagggagc caccaggccc ggcctccaga ggcaggagag tgtgttctga 1080

<210> 28
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met
 1 5 10 15
 Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
 20 25 30
 Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
 35 40 45
 Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
 50 55 60
 Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
 65 70 75 80
 Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
 85 90 95
 Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
 100 105 110
 Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
 115 120 125
 Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
 130 135 140
 Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg

145		150		155		160
Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe						
	165			170		175
Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val						
	180			185		190
Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile						
	195			200		205
Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu						
	210			215		220
Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala						
	225			230		235
Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val						
	245			250		255
Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr						
	260			265		270
His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu						
	275			280		285
Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu						
	290			295		300
Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr						
	305			310		315
Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu						
	325			330		335
Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu						
	340			345		350
Gln Arg Gln Glu Ser Val Phe						
	355					

<210> 29
 <211> 1503
 <212> DNA
 <213> Homo sapiens

 <400> 29

```

atggagcgtc cctgggagga cagcccaggc cgggaggggg cagctgaggg ctgcctgtg 60
ccagtcgccg cgggggcgcg ctccgggtgcc ggggcgagtg gcacaggctg gcagccatgg 120
gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgccgg ccctttgcgt 180
cgctggcccc cccctcgcc tgccagctcc agccccgccc cgggagcggc gtccgctcac 240
tcggttcaag gcagcgcgac tgcgggtggc gcacgaccag ggcgagacc ttgggggcgcg 300
cggcccatgg agtcggggct gctgcggcgc gcgcgggtga gcgaggtcat cgtcctgcat 360
tacaactaca ccggcaagct ccgcgggtgcg agctaccagc cgggtgccgg cctgcgcgcc 420
gacgccgtgg tgtgcctggc ggtgtgcgcc ttcctcgtgc tagagaatct agccgtgttg 480
ttggtgctcg gacgccaccc gcgcttccac gctcccatgt tctgctcct gggcagcctc 540
acgttgtcgg atctgctggc aggcgcgcgc tacgcgcga acatcctact gtcggggccg 600
ctcacgctga aactgtcccc cgcgctctgg ttgcacggg agggaggcgt cttcgtggca 660
ctcactgctg ccgtgctgag cctcctggcc atcgcgctgg agcgagcct caccatggcg 720
cgcagggggc ccgcgcccg ctccagtcgg gggcgacgc tggcgatggc agccgcggcc 780
tggggcgtgt cgctgctcct cgggctcctg ccagcgtgg gctggaattg cctgggtcgc 840
ctggacgctt gctccactgt cttgccgctc tacgccaaag cctacgtgct cttctgcgtg 900
ctgccttcg tggcatcct ggccgcgatc tgtgcaactc acgcgcgcac ctactgccag 960
gtacgcgcca acgcgcggcg cctgccggca cggcccgga ctgcggggac cacctcgacc 1020
cgggcgcgtc gcaagccgcg ctctctggcc ttgctgcgca cgcacagcgt ggtgctcctg 1080
gcctttgtgg catgttggg cccctcttc ctgctgctgt tgctcgacgt ggcggtgccg 1140
gcgcgacact gtctgtact cctgcaggcc gatcccttc tgggactggc catggccaac 1200
tcacttctga accccatcat ctacacgctc accaaccgcg acctgcgcca cgcgctcctg 1260
cgcctggtct gctgcggacg ccactcctgc ggcagagacc cgagtggctc ccagcagtcg 1320
gcgagcgcgg ctgaggcttc cgggggcctg cgcgcgtgcc tgcggcggg ccttgatggg 1380
agcttcagcg gctcggagcg ctcatcgccc cagcgcgacg ggctggacac cagcggctcc 1440
acaggcagcc ccggtgcacc cacagccgcc cggactctgg tatcagaacc ggctgcagac 1500
tga 1503

```

<210> 30
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
 1 5 10 15
 Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
 20 25 30
 Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
 35 40 45
 Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
 50 55 60
 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
 65 70 75 80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg
85 90 95

Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro
100 105 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg
115 120 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val
130 135 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu
145 150 155 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu
165 170 175

Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala
180 185 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala
195 200 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser
210 215 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala
225 230 235 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met
245 250 255

Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala
260 265 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu
275 280 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val
290 295 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln
305 310 315 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly
325 330 335

Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu
340 345 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro
355 360 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys
370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn
385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg
405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg
420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly
435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly
450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser
465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu
485 490 495

Pro Ala Ala Asp
500

<210> 31
<211> 1029
<212> DNA
<213> Homo sapiens

<400> 31
atgcaagccg tcgacaatct cacctotgcg cctgggaaca ccagtctgtg caccagagac 60
tacaaaatca ccaggtcct ctccactg ctctacactg tcctgtttt tgttgactt 120
atcacaaatg gcctggcgat gaggattttc tttcaaattc ggagtaaata aaactttatt 180
attttttctta agaacacagt catttctgat ctctcatga ttctgacttt tccattcaaa 240
attcttagtg atgccaaact gggaacagga cactgagaa cttttgtgtg tcaagttacc 300
tccgtcatat tttattttcac aatgtatatc agtattttcat tcctgggact gataactatc 360
gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctcttgggg 420

gctaagattc tctctgttgt catctgggca ttcattgttct tactctcttt gcctaacatg 480
attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctcttt ccttaaatca 540
gagttcggtc tagtctggca tgaaatagta aattacatct gtcaagtcatt tttctggatt 600
aatttcttaa ttgttattgt atgttataca ctcattacaa aagaactgta ccggtcatac 660
gtaagaacga ggggtgtagg taaagtcccc aggaaaaagg tgaacgtcaa agttttcatt 720
atcattgctg tattctttat ttgttttgtt cctttccatt ttgcccgaat tccttacacc 780
ctgagccaaa cccgggatgt ctttgactgc actgctgaaa atactctgtt ctatgtgaaa 840
gagagcactc tgtgggtaac ttccttaaata gcatgcctgg atccgttcat ctattttttc 900
ctttgcaagt ccttcagaaa ttccttgata agtatgctga agtgccccaa ttctgcaaca 960
tctctgtccc aggacaatag gaaaaaagaa caggatggtg gtgacccaaa tgaagagact 1020
ccaatgtaa 1029

<210> 32
<211> 342
<212> PRT
<213> Homo sapiens

<400> 32
Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
1 5 10 15
Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
20 25 30
Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
35 40 45
Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
50 55 60
Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65 70 75 80
Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
85 90 95
Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
100 105 110
Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
115 120 125
Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140
Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
 165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
 180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
 195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
 210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
 225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
 245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
 260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
 275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
 290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
 305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
 325 330 335

Asn Glu Glu Thr Pro Met
 340

<210> 33

<211> 1077

<212> DNA

<213> Homo sapiens

<400> 33

atgtcgggtct gctaccgtcc cccagggaac gagacactgc tgagctggaa gacttcgcgg 60
 gccacaggca cagccttcc gctgctggcg gcgctgctgg ggctgcctgg caacggcttc 120
 gtggtgtgga gcttggcggg ctggcgccct gcacgggggc gaccgctggc ggccacgctt 180
 gtgctgcacc tggcgctggc cgacggcgcg gtgctgctgc tcacgccgct ctttgtggcc 240

```

ttcctgaccc ggcaggcctg gccgctgggc caggcgggct gcaaggcggg gtactacgtg 300
tgcgcgctca gcatgtacgc cagcgtgctg ctcaccggcc tgctcagcct gcagcgctgc 360
ctcgcagtcg cccgccccctt cctgggcgct cggctgcgca gcccgccctt ggcccgccgc 420
ctgctgctgg cgggtctggct ggccgcccctg ttgctcgccg tcccggccgc cgtctaccgc 480
cacctgtgga gggaccgcgt atgccagctg tgccaccgct cggcgggtcca cgcgcgcgcc 540
cacctgagcc tggagactct gaccgctttc gtgcttcctt tcgggctgat gctcggtctgc 600
tacagcgtga cgctggcacg gctgcggggc gcccgctggg gctccgggcg gcacggggcg 660
cgggtggggc ggctgggtgag cgccatcgtg cttgccttcg gcttgctctg ggccccctac 720
cacgcagtcg accttctgca ggcggtcgca gcgctggctc caccggaagg ggcttggcg 780
aagctggggc gagccggcca ggcggcgca gcgggaacta cggccttggc cttcttcagt 840
tctagcgtca acccggtgct ctacgtcttc accgctggag atctgctgcc ccgggcaggt 900
ccccgtttcc tcacgcggct cttcgaaggc tctggggagg cccgaggggg cgccgcctct 960
agggaaggga ccatggagct ccgaactacc cctcagctga aagtgggtgg gcagggccgc 1020
ggcaatggag acccgggggg tgggatggag aaggacggtc cggaatggga ccttttga 1077

```

<210> 34
 <211> 358
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp
 1 5 10 15
 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu
 20 25 30
 Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp
 35 40 45
 Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu
 50 55 60
 Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala
 65 70 75 80
 Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala
 85 90 95
 Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr
 100 105 110
 Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu
 115 120 125
 Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala
 130 135 140

Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg
145 150 155 160

His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val
165 170 175

His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu
180 185 190

Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu
195 200 205

Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg
210 215 220

Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr
225 230 235 240

His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu
245 250 255

Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly
260 265 270

Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr
275 280 285

Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu
290 295 300

Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser
305 310 315 320

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val
325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp
340 345 350

Gly Pro Glu Trp Asp Leu
355

<210> 35
<211> 1005
<212> DNA
<213> Homo sapiens

<400> 35

```
atgctgggga tcatggcatg gaatgcaact tgcaaaaact ggctggcagc agaggctgcc 60
ctggaaaagt actaccttc cattttttat gggattgagt tcgttggtggg agtccttgga 120
aataccattg ttgtttacgg ctacatcttc tctctgaaga actggaacag cagtaatat 180
tatctcttta acctctctgt ctctgactta gcttttctgt gcacctccc catgctgata 240
aggagttatg ccaatggaaa ctggatatat ggagacgtgc tctgcataag caaccgatat 300
gtgcttcatg ccaacctcta taccagcatt ctctttctca cttttatcag catagatcga 360
tacttgataa ttaagtatcc tttccgagaa caccttctgc aaaagaaaga gtttgctatt 420
ttaatctcct tggccatttg ggtttttagta accttagagt tactacctat acttcccctt 480
ataaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac 540
cccaactaca acctcattta cagcatgtgt ctaacactgt tggggttcct tattcctctt 600
tttgtgatgt gtttctttta ttacaagatt gctctcttcc taaagcagag gaataggcag 660
gttgctactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720
ttctctgtgc tttttacacc ctatcacgtc atgcggaatg tgaggatcgc ttcacgcctg 780
gggagttgga agcagtatca gtgcactcag gtcgcatca actcctttta cattgtgaca 840
cggccttttg ctttctgaa cagtgtcatc aaccctgtct tctattttct tttgggagat 900
cacttcaggg acatgctgat gaatcaactg agacacaact tcaaatccct tacatccttt 960
agcagatggg ctcatgaact cctactttca ttcagagaaa agtga 1005
```

<210> 36

<211> 334

<212> PRT

<213> Homo sapiens

<400> 36

```
Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
  1             5             10             15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
          20             25             30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
  35             40             45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
  50             55             60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
  65             70             75             80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
          85             90             95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
 100             105             110
```

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
 115 120 125
 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
 130 135 140
 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
 145 150 155 160
 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
 165 170 175
 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
 180 185 190
 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
 195 200 205
 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
 210 215 220
 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
 225 230 235 240
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
 245 250 255
 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
 260 265 270
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
 275 280 285
 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300
 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320
 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
 325 330

<210> 37
 <211> 1296
 <212> DNA
 <213> Homo sapiens

<400> 37

```

atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg 60
acgcggggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120
ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc 180
tttggcaatg ctctgggtgt ctacgtgggtg acccgcagca aggccatgcg caccgtcacc 240
aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300
gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg 360
gtgccatttg tccagtctac cgctgttggt acagaaatgc tcaactatgac ctgcattgct 420
gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga 480
agggctttca caatgctagg tgtgggtctg ctgggtggcag tcatcgtagg atcacccatg 540
tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc 600
tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgct 660
atcctcttcc tctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720
ctttggataa agaaaagagt tggggatggt tcagtgcctt gaactattca tggaaaagaa 780
atgtccaaaa tagccaggaa gaagaaacga gctgtcatta tgatgggtgac agtgggtggct 840
ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat 900
tttgaaggagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960
ggattttcca actccatctg taatcccat gtctatgcat ttatgaatga aaacttcaaa 1020
aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacia 1080
aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagttttc cctcagagag 1140
aatccagtgg aggaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200
tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa 1260
ctggctgaga attctccttt agacagtggg cattaa 1296

```

<210> 38

<211> 431

<212> PRT

<213> Homo sapiens

<400> 38

```

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
  1             5             10             15

```

```

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
      20             25             30

```

```

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
    35             40             45

```

```

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
    50             55             60

```

```

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
    65             70             75             80

```

```

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
    85             90             95

```

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
 100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
 115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
 130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
 145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
 165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
 180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
 195 200 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
 210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
 225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
 245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val
 260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
 275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
 290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
 305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
 325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
 340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
 355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
 370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
 385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
 405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
 420 425 430

<210> 39
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 39
 ctgtgtacag cagttcgcag agtg 24

<210> 40
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 40
 gagtgccagg cagagcaggt agac 24

<210> 41
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 41
 cccgaattcc tgcttgctcc cagcttggcc c 31

<210> 42
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 42
tgtggaatcct gctgtcaaag gtcccattcc gg 32

<210> 43
<211> 20
<212> DNA
<213> Homo sapiens

<400> 43
tcacaatgct aggtgtggtc 20

<210> 44
<211> 22
<212> DNA
<213> Homo sapiens

<400> 44
tgcatagaca atgggattac ag 22

<210> 45
<211> 511
<212> DNA
<213> Homo sapiens

<400> 45
tcacaatgct aggtgtggtc tggctggtgg cagtcacgt aggatcaccc atgtggcacg 60
tgcaacaact tgagatcaaa tatgacttcc tatatgaaaa ggaacacatc tgctgcttag 120
aagagtggac cagccctgtg caccagaaga tctacaccac cttcatcctt gtcacacctc 180
tctccttgcc tcttatggtg atgcttattc tgtacgtaaa attggttatg aactttggat 240
aaagaaaaga gttggggatg gttcagtgtc tcgaactatt catggaaaag aaatgtccaa 300
aatagccagg aagaagaaac gagctgtcat tatgatggtg acagtgggtg ctctctttgc 360
tgtgtgctgg gcaccattcc atgttgtcca tatgatgatt gaatacagta attttgaaaa 420
ggaatatgat gatgtcacia tcaagatgat ttttgctatc gtgcaaatta ttggattttc 480
caactccatc tgtaatccca ttgtctatgc a 511

<210> 46
<211> 21
<212> DNA
<213> Homo sapiens

<400> 46
ctgcttagaa gaggtagacca g 21

<210> 47
<211> 22
<212> DNA
<213> Homo sapiens

<400> 47
ctgtgcacca gaagatctac ac

22

<210> 48
<211> 21
<212> DNA
<213> Homo sapiens

<400> 48
caaggatgaa ggtggtgtag a

21

<210> 49
<211> 23
<212> DNA
<213> Homo sapiens

<400> 49
gtgtagatct tctggtgcac agg

23

<210> 50
<211> 21
<212> DNA
<213> Homo sapiens

<400> 50
gcaatgcagg tcatagtgag c

21

<210> 51
<211> 27
<212> DNA
<213> Homo sapiens

<400> 51
tggagcatgg tgacgggaat gcagaag

27

<210> 52
<211> 27

<212> DNA
<213> Homo sapiens

<400> 52
gtgatgagca ggctactgag cgccaag

27

<210> 53
<211> 23
<212> DNA
<213> Homo sapiens

<400> 53
gcaatgcagg cgcttaacat tac

23

<210> 54
<211> 22
<212> DNA
<213> Homo sapiens

<400> 54
ttgggttaca atctgaaggg ca

22

<210> 55
<211> 23
<212> DNA
<213> Homo sapiens

<400> 55
actccgtgtc cagcaggact ctg

23

<210> 56
<211> 24
<212> DNA
<213> Homo sapiens

<400> 56
tgcgtgttcc tggaccctca cgtg

24

<210> 57
<211> 29
<212> DNA
<213> Homo sapiens

<400> 57
caggccttgg attttaatgt cagggatgg

29

<210> 58
<211> 27
<212> DNA
<213> Homo sapiens

<400> 58
ggagagtcag ctctgaaaga attcagg

27

<210> 59
<211> 27
<212> DNA
<213> Homo sapiens

<400> 59
tgatgtgatg ccagatacta atagcac

27

<210> 60
<211> 27
<212> DNA
<213> Homo sapiens

<400> 60
cctgattcat ttaggtgaga ttgagac

27

<210> 61
<211> 21
<212> DNA
<213> Homo sapiens

<400> 61
gacaggtacc ttgccatcaa g

21

<210> 62
<211> 22
<212> DNA
<213> Homo sapiens

<400> 62
ctgcacaatg ccagtataa gg

22

<210> 63
<211> 27
<212> DNA
<213> Homo sapiens

<400> 63
ctgactttctt gttcctggca gcagcgg

27

<210> 64
<211> 27
<212> DNA
<213> Homo sapiens

<400> 64
agaccagcca gggcacgctg aagagtg

27

<210> 65
<211> 32
<212> DNA
<213> Homo sapiens

<400> 65
gatcaagctt ccatactact gaaaccatgg tc

32

<210> 66
<211> 35
<212> DNA
<213> Homo sapiens

<400> 66
gatcagatct cagttccaat attcacacca ccgtc

35

<210> 67
<211> 22
<212> DNA
<213> Homo sapiens

<400> 67
ctggtgtgct ccatggcatc cc

22

<210> 68
<211> 22

<212> DNA
<213> Homo sapiens

<400> 68
gtaagcctcc cagaacgaga gg

22

<210> 69
<211> 24
<212> DNA
<213> Homo sapiens

<400> 69
cagcgcaggg tgaagcctga gagg

24

<210> 70
<211> 24
<212> DNA
<213> Homo sapiens

<400> 70
ggcacctgct gtgacctgtg cagg

24

<210> 71
<211> 22
<212> DNA
<213> Homo sapiens

<400> 71
gtcctgccac ttcgagacat gg

22

<210> 72
<211> 23
<212> DNA
<213> Homo sapiens

<400> 72
gaaacttctc tgcccttacc gtc

23

<210> 73
<211> 26
<212> DNA
<213> Homo sapiens

